



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 142420

To: Janet Epps-Ford
Location: REM/2C05/2C18
Art Unit: 1635
Tuesday, January 18, 2005

Case Serial Number: 09/733306

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

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From: Epps-Ford, Janet
Sent: Wednesday, January 12, 2005 12:45 PM
To: STIC-Biotech/ChemLib
Subject: Protein Sequence Search

Please search SEQ ID NO: 4 of application 09/733,306 in all commercial amino acid databases and all published us patent amino acid databases.

4-312 aa

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

____ STIC
____ CM-1
____ Pre-S

Type of Search

____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors

____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
✓ Other CGN

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2005, 15:40:37 ; Search time 156 Seconds
(without alignments)
717.459 Million cell updates/sec

Title: US-09-733-306C-4
Perfect score: 1573
Sequence: 1 MANNDVAVLKRLLEQKGAEADQ.....FEVKGKGVCRQAQTMSNSGIK 312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1573	100.0	312	5	ABB07442	Abb07442 Human p43
2	1573	100.0	312	6	AAO29575	Aao29575 Human Pc2
3	1573	100.0	312	8	ADH74487	Adh74487 Human wou
4	1573	100.0	312	8	ADP85653	Adp85653 Human end
5	1573	100.0	328	4	AAB63244	Aab63244 Human bre
6	1343	85.4	310	2	AAR72577	Aar72577 Mouse EMA
7	831	52.8	166	6	ABU10452	Abu10452 Immunolog
8	823	52.3	166	2	AAW14561	Aaw14561 Endotheli
9	709	45.1	147	6	ABU10250	Abu10250 Immunolog
10	671	42.7	294	4	ABB59210	Abb59210 Drosophil
11	522.5	33.2	280	7	ABM74361	Abm74361 DNA clone
12	522.5	33.2	289	7	ABM73655	Abm73655 DNA clone
13	516	32.8	108	6	ABU10451	Abu10451 Immunolog
14	510.5	32.5	659	5	AAE19811	Aae19811 Corn p012
15	507	32.2	95	8	ADN99968	Adn99968 Novel hum
16	499	31.7	797	8	ADN73157	Adn73157 Thale cre
17	451	28.7	536	4	AAB47611	Aab47611 Human ful
18	451	28.7	536	5	AAE13487	Aae13487 Human tyr
19	451	28.7	536	6	ABU72380	Abu72380 Human ful
20	450	28.6	528	7	ADF76697	Adf76697 Novel hum
21	450	28.6	528	8	ADN05830	Adn05830 Antipsori
22	449.5	28.6	527	7	ABU64299	Abu64299 Human tyr
23	440.5	28.0	301	2	AAW53962	Aaw53962 Monocyte
24	440.5	28.0	301	8	ADE76967	Ade76967 Human pro
25	430.5	27.4	178	4	AAB47613	Aab47613 Human Tyr

Epps-Ford
09/7333306
seq. ID 4 w/interf

26	430.5	27.4	178	5	AAE13489	Aae13489 Human Tyr
27	430.5	27.4	178	6	ABU72382	Abu72382 Human Tyr
28	429.5	27.3	168	2	AAW06596	Aaw06596 Human end
29	429.5	27.3	168	3	AAy69674	Aay69674 Human end
30	400.5	25.5	382	3	AAG31613	Aag31613 Arabidops
31	400.5	25.5	389	3	AAG31612	Aag31612 Arabidops
32	400.5	25.5	440	3	AAG31611	Aag31611 Arabidops
33	395	25.1	525	4	ABB60745	Abb60745 Drosophil
34	391.5	24.9	265	7	ABM74280	Abm74280 DNA clone
35	343	21.8	273	3	AAG08528	Aag08528 Arabidops
36	294	18.7	123	8	ADN99487	Adn99487 Novel hum
37	293	18.6	58	6	ABU72393	Abu72393 Human pro
38	227	14.4	720	6	ADA33478	Ada33478 Acinetoba
39	225	14.3	690	6	ABU16644	Abu16644 Protein e
40	223.5	14.2	737	4	AAB96809	Aab96809 Putative
41	221.5	14.1	744	8	ADN46653	Adn46653 Thermococ
42	198.5	12.6	234	4	ABG22608	Abg22608 Novel hum
43	197.5	12.6	545	4	ABG17833	Abg17833 Novel hum
44	197	12.5	276	4	ABG26195	Abg26195 Novel hum
45	188.5	12.0	669	6	ABU29885	Abu29885 Protein e

ALIGNMENTS

RESULT 1
ABB07442
ID ABB07442 standard; protein; 312 AA.

XX ABB07442;

DT 23-APR-2002 (first entry)

XX Human p43 polypeptide.

KW Human; p43; cytostatic; anti-tumour; anti-angiogenic; EMAP II; cytokine;
chemotaxis.

XX Homo sapiens.

Key Domain	Location/Qualifiers
FT	1..146 /note= "N-terminal domain"
FT	10..21 /note= "beta1 strand"
FT	28..34 /note= "beta2 strand"
FT	40..46 /note= "beta3 strand"
FT	53..56 /note= "alpha 1 helix"
FT	59..66 /note= "beta4 strand"
FT	70..72 /note= "beta5i strand"
FT	75..77 /note= "beta6i strand"
FT	79..85 /note= "beta7 strand"
FT	90..92 /note= "beta8 strand"
FT	103..106 /note= "beta9 strand"
FT	119..123 /note= "alpha 2 helix"
FT	124..130 /note= "alpha 3 helix"
FT	132..134 /note= "beta10 strand"
FT	140..142 /note= "beta11 strand"
FT	147..312 /note= "C-terminal domain"

XX WO200195927-A1.
PN
XX
XX 20-DEC-2001.
PD
XX
XX 14-JUN-2000; 2000WO-KR0000630.
PF
XX
XX 14-JUN-2000; 2000WO-KR0000630.
PR
XX
XX (IMAG-) IMAGE CO LTD.
PA
XX
XX Kim S, Ko Y, Kim YS, Jo YJ;
PI
XX
XX WPI; 2002-098017/13.
DR
XX N-PSDB; ABA94640.
DR
XX
XX Novel anti-tumor and anti-angiogenic agent of p43 comprises N-terminal
PT domain and C-terminal domain containing eleven beta-strands forming a
PT structural core and three flanking alpha-helices.
PT
XX
XX Claim 1; Fig 1; 35pp; English.
PS
XX
XX The invention provides an anti-tumour and anti-angiogenic agent of p43
CC consisting of two domains, the N-terminal domain (146 amino acids) and C-
CC terminal domain (166 amino acids) containing 11 beta-strands forming a
CC structural core and 3 flanking alpha-helices. p43 is useful as an anti -
CC tumour and anti-angiogenic agent. p43 and its C-terminal cytokine domain
CC (EMAP II) induce regression of fibrosarcoma in immunocompromised mouse
CC while its N-terminal domain does not. p43 is a potent cytokine as
CC determined by the induction of tumour necrosis factor-alpha (TNF-alpha),
CC interleukin-6 (IL-6), IL-8 and matrix metalloprotease-9 or by its
CC activity of chemotaxis. The present sequence represents the human p43
CC polypeptide
XX
SQ Sequence 312 AA;
Query Match 100.0%; Score 1573; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.5e-135;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANNDVAVLKRLEQKGAEDQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKEIE 60
Db 1 MANNDVAVLKRLEQKGAEDQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKEIE 60
Qy 61 ELKQELIQAEIQNGVKQIAFPSPGTPPLHANSVMSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
Db 61 ELKQELIQAEIQNGVKQIAFPSPGTPPLHANSVMSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
Qy 121 KKAKEKIEKKEKKEKQKQSIAGSADSKPIDVSRDLRLIGCIITARKHPDADSLYVEEVD 180
Db 121 KKAKEKIEKKEKKEKQKQSIAGSADSKPIDVSRDLRLIGCIITARKHPDADSLYVEEVD 180
Qy 181 VGEIAPRTVVSGLVNHPVLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
Db 181 VGEIAPRTVVSGLVNHPVLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
Qy 241 PPNGSVPGDRITFDAPFGPEPKELNPKKKIWEQIQPDLHTNDECVAITYKGVPEVKGKV 300
Db 241 PPNGSVPGDRITFDAPFGPEPKELNPKKKIWEQIQPDLHTNDECVAITYKGVPEVKGKV 300
Qy 301 CRAQTMNSNGIK 312
Db 301 CRAQTMNSNGIK 312
RESULT 2
AAO29575
ID AAO29575 standard; protein; 312 AA.
XX
AC AAO29575;
XX
DT 27-AUG-2003 (first entry)
XX

DE Human Pc240 protein.
XX
KW Human; differentially regulated protein; prevention; therapy; vaccine;
KW prostate cancer; endothelial monocyte activating polypeptide II;
KW gene therapy; Pc240.
XX
OS Homo sapiens.
XX
XX WO2003040331-A2.
PN
XX
XX 15-MAY-2003.
PD
XX
XX 07-NOV-2002; 2002WO-US035563.
PF
XX
XX 07-NOV-2001; 2001US-0331041P.
PR
XX 07-NOV-2001; 2001US-0331042P.
PR
XX 18-DEC-2001; 2001US-0340251P.
PR
XX 07-JAN-2002; 2002US-0344791P.
XX
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
PA
XX
XX Sun Z, Li X, Jay G, Kovacs KF, Fan W;
PI
XX
XX WPI; 2003-449451/42.
DR
XX N-PSDB; AAL60070.
DR
XX
XX New polynucleotide for diagnosing, staging, monitoring, prognosticating,
PT preventing or treating, or determining the predisposition to, diseases or
PT conditions such as prostate cancer, and for research or forensic science.
PT
XX
XX Disclosure; Page 183-184; 100pp; English.
PS
XX
XX The present invention relates to novel differentially regulated genes and
CC polypeptides encoded by them. Sequences of the invention are useful in
CC diagnosing, staging, monitoring, prognosticating, preventing, treating or
CC determining the predisposition to diseases or conditions such as prostate
CC cancer. They may be used as molecular markers, drug targets, vaccines, in
CC gene therapy, research, clinical medicine or forensic science. The
CC present sequence is a differentially regulated prostate protein
CC (endothelial monocyte activating polypeptide II), Pc240
XX
SQ Sequence 312 AA;
Query Match 100.0%; Score 1573; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.5e-135;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANNDVAVLKRLEQKGAEDQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKEIE 60
Db 1 MANNDVAVLKRLEQKGAEDQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKEIE 60
Qy 61 ELKQELIQAEIQNGVKQIAFPSPGTPPLHANSVMSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
Db 61 ELKQELIQAEIQNGVKQIAFPSPGTPPLHANSVMSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
Qy 121 KKAKEKIEKKEKKEKQKQSIAGSADSKPIDVSRDLRLIGCIITARKHPDADSLYVEEVD 180
Db 121 KKAKEKIEKKEKKEKQKQSIAGSADSKPIDVSRDLRLIGCIITARKHPDADSLYVEEVD 180
Qy 181 VGEIAPRTVVSGLVNHPVLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
Db 181 VGEIAPRTVVSGLVNHPVLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
Qy 241 PPNGSVPGDRITFDAPFGPEPKELNPKKKIWEQIQPDLHTNDECVAITYKGVPEVKGKV 300
Db 241 PPNGSVPGDRITFDAPFGPEPKELNPKKKIWEQIQPDLHTNDECVAITYKGVPEVKGKV 300
Qy 301 CRAQTMNSNGIK 312
Db 301 CRAQTMNSNGIK 312
RESULT 3

ADH74487
ID ADH74487 standard; protein; 312 AA.
XX
AC ADH74487;
XX
DT 15-APR-2004 (first entry)
XX
DE Human wound healing stimulating polypeptide p43, SEQ ID 1.
XX
KW Vulneryary; antiulcer; dermatological; antiallergic; antiinflammatory;
wound healing; burn; ulcer; trauma; post-surgical; post-child birth;
KW chronic wound; dermatitis; sunburn; chemical burn; radiation burn;
KW thermal burn; pressure ulcer; plaster ulcer; decubitus ulcer; bedsores;
KW pressure sore; diabetes; poor circulation; impetigo; intertrigo;
KW folliculitis; eczema; p43.
XX
OS Homo sapiens.
XX
PN EP1384486-A1.
XX
PD 28-JAN-2004.
XX
XX
PF 22-JUL-2003; 2003EP-00016724.
XX
XX
PR 22-JUL-2002; 2002KR-00042858.
XX
XX
PA (UYSE-) UNIV SEOUL NAT IND FOUND.
XX
PI Kim S;
XX
XX
DR WPI; 2004-145613/15.
XX
XX
PT Use of p43 polypeptide, for the manufacture of pharmaceutical composition
PT intended to stimulate wound healing in a subject.
XX
PS Claim 1; SEQ ID NO 1; 20pp; English.
XX
CC The invention relates to the use of one or more polypeptides (I) chosen
CC from a polypeptide having a fully defined p43 sequence of 312 amino acids
CC as given in the specification and a polypeptide having 70% or more
CC sequence homology with (S1), for the manufacture of the pharmaceutical
CC composition (II) which is intended to stimulate wound healing in a
CC subject. The polypeptide of the invention is useful for the manufacture
CC of the pharmaceutical composition (II) which is intended to stimulate
CC wound healing in a subject. The wound is chosen from burn, ulcer, trauma,
CC post-surgical, post-child birth, chronic wound and dermatitis. The burn
CC is chosen from sun burn, chemical burn, radiation burn, and thermal burn.
CC The ulcer is chosen from pressure ulcer, plaster ulcer and decubitus
CC ulcer. The chronic wound is chosen from bedsores, pressure sores,
CC diabetes-related and poor circulation-related. The dermatitis is chosen
CC from impetigo, intertrigo, folliculitis and eczema. The current sequence
CC represents the wound healing stimulating polypeptide of the invention.
XX
SQ Sequence 312 AA;

Query Match 100.0%; Score 1573; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.5e-135;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANNDVLRLEQKGAADQII EYLKQQVSLKKEKAILQATLREEKKLRVENAKLKEIE 60
DB 1 MANNDVLRLEQKGAADQII EYLKQQVSLKKEKAILQATLREEKKLRVENAKLKEIE 60

QY 61 ELKQELIQAEIQNGVKQIAFPSPGTPPLHANSMVSENVIOSTAVTTVSSGTKEQIKGGTGDE 120
DB 61 ELKQELIQAEIQNGVKQIAFPSPGTPPLHANSMVSENVIOSTAVTTVSSGTKEQIKGGTGDE 120

QY 121 KKAKEKIEKKGEKKEKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
DB 121 KKAKEKIEKKGEKKEKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180

QY 181 VGEIAPRTVSVGLVNHVPLEQMQRNVILLCNLKPAKMRGVLSQLMVCASSPEKIEILA 240
|||||

Db 181 VGEIAPRTVSVGLVNHVPLEQMQRNVILLCNLKPAKMRGVLSQLMVCASSPEKIEILA 240
QY 241 PPNGSVPGDRITFDAPFGPEPKELNPKKKIWEQIQPDLHTNDECVAITYKGVPEVKGKV 300
|||||
Db 241 PPNGSVPGDRITFDAPFGPEPKELNPKKKIWEQIQPDLHTNDECVAITYKGVPEVKGKV 300
QY 301 CRAQTMNSGIK 312
|||||
Db 301 CRAQTMNSGIK 312

RESULT 4
ADP85653
ID ADP85653 standard; protein; 312 AA.
XX
AC ADP85653;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human endothelial monocyte-activating polypeptide-II (EMAP-II).
XX
KW EMAP-II; endothelial monocyte-activating polypeptide-II; EMAP-2; SCYE1;
KW small inducible cytokine subfamily E member 1;
KW hyperproliferative disorder; cancer; gene therapy; human.
XX
OS Homo sapiens.
XX
PN US2004110144-A1.
XX
PD 10-JUN-2004.
XX
XX
PF 09-DEC-2002; 2002US-00316232.
XX
PR 09-DEC-2002; 2002US-00316232.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dean NM, Dobie KW;
XX
DR WPI; 2004-440333/41.
DR N-PSDB; ADP85584.
XX
PT New oligonucleotide compound that inhibits expression of EMAP-II, useful
PT for preparing a composition for treating hyperproliferative disorder,
PT e.g. cancer.
XX
PS Disclosure; Page 22-23; 35pp; English.
XX
CC The present invention relates to a compounds, compositions and methods
CC for modulating the expression of endothelial monocyte-activating
CC polypeptide-II (EMAP-II). EMAP-II is also known as EMAP-2, small
CC inducible cytokine subfamily E, member 1 (SCYE1). The compound comprises
CC antisense oligonucleotides targeted to EMAP-II. The invention is useful
CC for preparing a composition for treating hyperproliferative disorder e.g.
CC cancer. It is also useful in gene therapy. The present sequence is human
CC endothelial monocyte-activating polypeptide-II (EMAP-II). This sequence
CC is used in the invention.
XX
SQ Sequence 312 AA;

Query Match 100.0%; Score 1573; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.5e-135;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANNDVLRLEQKGAADQII EYLKQQVSLKKEKAILQATLREEKKLRVENAKLKEIE 60
DB 1 MANNDVLRLEQKGAADQII EYLKQQVSLKKEKAILQATLREEKKLRVENAKLKEIE 60

QY 61 ELKQELIQAEIQNGVKQIAFPSPGTPPLHANSMVSENVIOSTAVTTVSSGTKEQIKGGTGDE 120
DB 61 ELKQELIQAEIQNGVKQIAFPSPGTPPLHANSMVSENVIOSTAVTTVSSGTKEQIKGGTGDE 120

QY 121 KKAKEKIEKKGEKKEKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
|||||

Db 121 KKAKEKIEKKKEKKQQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
QY 181 VGEIAPRTVTVSGLVNHVPLEQMQNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
Db 181 VGEIAPRTVTVSGLVNHVPLEQMQNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
QY 241 PPNGSVPGDRITFDAPFGEPEKELNPKKKIWEQIQPDLHTNDECVAATYKGVFFEVKGKV 300
Db 241 PPNGSVPGDRITFDAPFGEPEKELNPKKKIWEQIQPDLHTNDECVAATYKGVFFEVKGKV 300
QY 301 CRAQTMSNSGIK 312
Db 301 CRAQTMSNSGIK 312
RESULT 5
AAB63244
ID AAB63244 standard; protein; 328 AA.
XX
AC AAB63244;
XX
DT 26-MAR-2001 (first entry)
XX Human breast cancer associated antigen protein sequence SEQ ID NO:606.
DE Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
XX cancer associated antigen; cytostatic; cancer vaccine.
KW
KW
XX Homo sapiens.
OS
XX
XX WO200073801-A2.
XX
PD 07-DEC-2000.
XX
XX 26-MAY-2000; 2000WO-US014749.
PF
XX
XX 28-MAY-1999; 99US-0136526P.
PR 10-SEP-1999; 99US-0153454P.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX
XX Obata Y;
PI
XX
XX WPI; 2001-025274/03.
DR
XX Nucleic acids encoding breast, gastric and prostate cancer associated
PT antigen precursors, useful for diagnosing and treating a condition
PT characterized by expression of an abnormal amount of a protein, e.g.
PT cancer.
XX
XX Example 1; Page 478; 799pp; English.
PS
XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC represent nucleotide sequences encoding human breast, gastric and
CC prostate cancer associated antigen precursors (CAAP) respectively.
CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC represent human breast, gastric and prostate CAAP protein sequence
CC respectively. CAAPs have cytostatic activity and can be used in the
CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC condition characterised by expression of an abnormal amount of a protein,
CC e.g. cancer
XX
SQ Sequence 328 AA;
Query Match 100.0%; Score 1573; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.6e-135;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANNDVAVLKRLEQKGAEADQIIIEYLKQQVSLKKEKAILQATLRREKKLRVENAKLKEIE 60
Db 17 MANNDVAVLKRLEQKGAEADQIIIEYLKQQVSLKKEKAILQATLRREKKLRVENAKLKEIE 76

QY 61 ELKQELIQAEIQNGVKQIAFPSTPLHANSMVSENVIOSTAVTTVSSGTKEIQIKGGTGDE 120
Db 77 ELKQELIQAEIQNGVKQIAFPSTPLHANSMVSENVIOSTAVTTVSSGTKEIQIKGGTGDE 136
QY 121 KKAKEKIEKKKEKKQQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
Db 137 KKAKEKIEKKKEKKQQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 196
QY 181 VGEIAPRTVTVSGLVNHVPLEQMQNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
Db 197 VGEIAPRTVTVSGLVNHVPLEQMQNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 256
QY 241 PPNGSVPGDRITFDAPFGEPEKELNPKKKIWEQIQPDLHTNDECVAATYKGVFFEVKGKV 300
Db 257 PPNGSVPGDRITFDAPFGEPEKELNPKKKIWEQIQPDLHTNDECVAATYKGVFFEVKGKV 316
QY 301 CRAQTMSNSGIK 312
Db 317 CRAQTMSNSGIK 328
RESULT 6
AAR72577
ID AAR72577 standard; protein; 310 AA.
XX
AC AAR72577;
XX 25-MAR-2003 (revised)
DT 29-SEP-1995 (first entry)
DT
XX Mouse EMAPII.
DE
XX
KW EMAPII; endothelial monocyte activating polypeptide II; chemotaxis;
XX inflammation; tissue factor; tumor; cancer; therapy; methA; sarcoma.
OS Mus musculus.
XX
XX WO9509180-A1.
PN
XX 06-APR-1995.
PD
XX
XX 29-SEP-1994; 94WO-US011085.
PF
XX 29-SEP-1993; 93US-00129456.
PR
XX (UYCO) UNIV COLUMBIA NEW YORK.
PA Stern DM, Clauss M, Kao J, Kayton M, Libutti SK;
PI WPI; 1995-147389/19.
XX N-PSDB; AAQ86718.
DR
XX New endothelial monocyte activating polypeptide II - induces chemotaxis,
PT inflammation and tissue factor, useful for treating tumours, also related
PT antibodies, DNA and active fragments.
XX
PS Disclosure; Fig 4; 180pp; English.
XX
CC A mouse methA sarcoma cDNA library was screened with a probe based on the
CC N-terminal sequence of mouse EMAPII. Overlapping clones were combined to
CC obtain a contiguous full-length sequence (given in AAQ86718) encoding a 33
CC kDa protein (AAR72577). Recombinant EMAPII was expressed in E. coli.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 310 AA;
Query Match 85.4%; Score 1343; DB 2; Length 310;
Best Local Similarity 85.9%; Pred. No. 1.9e-114;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;
QY 1 MANNDVAVLKRLEQKGAEADQIIIEYLKQQVSLKKEKAILQATLRREKKLRVENAKLKEIE 60

Db 1 MATNDAVLKRLEQGAADQIIIEYLKQQVALLKEKAILQATMREEKKLRVENAKLKEIE 60

QY 61 ELKQELIQAEIQNGVKQIAFPSTGLHANSMVSENVISTAV-TTVSSGTKEIQKGGTGD 119

Db 61 ELKQELILAEIHNGVEQVRRLSTPLQTNCTASESVVQSPSVAATTASPATKEQIK--AGE 118

QY 120 EKKAKEKIEKGEKKEKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEV 179

Db 119 EKKVKEKTEKGEKKE-KQSSAAASTDSKPIDASRLDLRIGCIIVTAKHPDADSLYVEEV 177

QY 180 DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLQAMVMCASSPEKIEIL 239

Db 178 DVGEAAPRTVVSGLVNHVPLEQMQNRMVLLCNLKPAKMRGVLQAMVMCASSPEKVEIL 237

QY 240 APPNGSVPGDRITFDAPFGPEPKELNPKKIWEIQIOPDLHTNDECVTATYKGVPEVKKG 299

Db 238 APPNGSVPGDRITFDAPFGPEPKELNPKKIWEIQIOPDLHTNAECVTATYKGAPFEVKKG 297

QY 300 VCRAQTMSNSGIK 312

Db 298 VCRAQTMANSGIK 310

RESULT 7

ABU10452

ID ABU10452 standard; protein; 166 AA.

XX AC ABU10452;

XX DT 01-AUG-2003 (first entry)

XX DE Immunological enhancement agent p43 (91-256).

XX KW Immunostimulant; cytokine agonist; p43; cytokine; interleukin-8; TNF; tumour necrosis factor.

XX OS Mammalia.

XX PN US2003004309-A1.

XX PD 02-JAN-2003.

XX PF 16-AUG-2001; 2001US-00930169.

XX PR 05-JUN-2001; 2001KR-00031310.

XX PA (KIMS/) KIM S.

XX PA (KOY/) KO Y.

XX PI Kim S, Ko Y;

XX DR WPI; 2003-447359/42.

XX PT New immunological enhancement agent comprising an N-terminal peptide of p43, useful for increasing the amount of tumor necrosis factor and interleukin-8 to improve the immune response.

XX PS Claim 3; Page 5; 12pp; English.

XX CC The present sequence represents an immunological enhancement agent comprising an N-terminal peptide of p43. The peptide can act as a cytokine to increase the amount of tumour necrosis factor (TNF) and interleukin-8 useful for improving an immune response and used as an immunological enhancement agent. The present sequence represents the amino acid sequence of the immunological enhancement agent p43 (91-256)

SQ Sequence 166 AA;

Query Match 52.8%; Score 831; DB 6; Length 166;

Best Local Similarity 100.0%; Pred. No. 7.4e-68;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 MVSENVISTAVTTVSSGTKEIQKGGTGDEKKAKEKIEKKGEKKEKKQSQIAGSADSKPI 150

Db 1 MVSENVISTAVTTVSSGTKEIQKGGTGDEKKAKEKIEKKGEKKEKKQSQIAGSADSKPI 60

QY 151 DVSRLDLRIGCIITARKHPDADSLYVEEVVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILL 210

Db 61 DVSRLDLRIGCIITARKHPDADSLYVEEVVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILL 120

QY 211 CNLKPAKMRGVLQAMVMCASSPEKIEILAPPNGSVPGDRITFDAF 256

Db 121 CNLKPAKMRGVLQAMVMCASSPEKIEILAPPNGSVPGDRITFDAF 166

RESULT 8

AAW14561

ID AAW14561 standard; protein; 166 AA.

XX AC AAW14561;

XX DT 01-DEC-1997 (first entry)

XX DE Endothelial monocyte activating polypeptide II.

XX KW EMAP-II; inhibitor; endothelial cell formation; blood vessel; retinopathy; tumour; subcutaneous; intraperitoneal; intravenous; intracranial; intratumoural; carcinoma; glioblastoma; positive pressure microinfusion; aortic cell; angiogenesis; eye disease; diabetes; sickle cell anaemia; prematurity; age-related macular degeneration.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /label= Ser, Met, Gly

FT Misc-difference 15 /label= Cys, Arg

XX PN W09710841-A1.

XX PD 27-MAR-1997.

XX PF 18-SEP-1996; 96WO-US015007.

XX PR 18-SEP-1995; 95US-0003898P.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Stern D, Schwarz M;

XX DR WPI; 1997-202617/18.

XX PT Treatment of tumours with endothelial monocyte activating peptide II - also used to inhibit growth of endothelial cells and formation of blood vessels, e.g. in retinopathy.

XX PS Claim 13; Page 73; 104pp; English.

XX CC A method has been developed for the treatment of tumours. The method involves subcutaneous, intraperitoneal, intravenous, intracranial or intratumoural administration of an endothelial monocyte activating polypeptide II (EMAP-II), or a EMAP-II-derived polypeptide. The present sequence represents murine EMAP-II which can be used to produce the EMAP-II-derived polypeptide as long as it contains at least ninety percent homology to the present sequence. The method is especially used to treat carcinoma (administered intraperitoneally) or glioblastoma (administered intratumourally by positive pressure microinfusion). Inhibition of endothelial cell growth is particularly applied to aortic cells and inhibition of angiogenesis to treatment of eye diseases associated with excessive blood vessel formation, especially retinopathy (diabetic, related to sickle cell anaemia, retinopathy of prematurity or age-related macular degeneration). Intraperitoneal administration allows tumours too small (not over 2 mm in diameter) for intratumoural injection to be treated before they grow larger

XX Sequence 166 AA;
SQ
Query Match 52.3%; Score 823; DB 2; Length 166;
Best Local Similarity 93.9%; Pred. No. 4e-67;
Matches 155; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 148 KPIDVSRDLRIGCIITARKHPDADSLYVEEDVGEIAPRTVSGLVNHPLEQMQRNV 207
Db 2 KPIDASRLDLRIGXIVTAKKHPDADSLYVEEDVGEAAPRTVSGLVNHPLEQMQRNV 61
QY 208 ILLCNLKPAMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAPPGEKELNPK 267
Db 62 VLLCNLKPAMRGVLSQAMVMCASSPEKVEILAPPNGSVPGDRITFDAPPGEKELNPK 121
QY 268 KKIWEQIQPDLHTNDEC VATYKGVPPFEVKGKVCRAQTMNSGIK 312
Db 122 KKIWEQIQPDLHTNAECVATYKGAPFEVKGKVCRAQTMANSGIK 166

RESULT 9
ABU10250
ID ABU10250 standard; protein; 147 AA.
XX
AC ABU10250;
XX
DT 01-AUG-2003 (first entry)
XX
DE Immunological enhancement agent p43 (1-147).
XX
KW Immunostimulant; cytokine agonist; p43; cytokine; interleukin-8; TNF;
KW tumour necrosis factor.
XX
OS Mammalia.
XX
PN US2003004309-A1.
XX
PD 02-JAN-2003.
XX
PF 16-AUG-2001; 2001US-00930169.
XX
PR 05-JUN-2001; 2001KR-00031310.
XX
PA (KIMS/) KIM S.
PA (KOYY/) KO Y.
XX
PI Kim S, Ko Y;
XX
DR WPI; 2003-447359/42.
XX
PT New immunological enhancement agent comprising an N-terminal peptide of
PT p43, useful for increasing the amount of tumor necrosis factor and
PT interleukin-8 to improve the immune response.
XX
PS Claim 1; Page 4; 12pp; English.
XX

The present sequence represents an immunological enhancement agent comprising an N-terminal peptide of p43. The peptide can act as a cytokine to increase the amount of tumour necrosis factor (TNF) and interleukin-8 useful for improving an immune response and used as an immunological enhancement agent. The present sequence represents the amino acid sequence of the immunological enhancement agent p43 (1-147)
XX
SQ Sequence 147 AA;
Query Match 45.1%; Score 709; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 9.8e-57;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANNDVLRLEQKGAADQIIIEYLKQVSLLEKAILQATLREEKKLRVENAKLKEIE 60
Db 1 MANNDVLRLEQKGAADQIIIEYLKQVSLLEKAILQATLREEKKLRVENAKLKEIE 60

QY 61 ELKQELIQAEIQNGVKQIAFPSTGTPHLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
Db 61 ELKQELIQAEIQNGVKQIAFPSTGTPHLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
QY 121 KKAKEKIEKKGKKEKKQQSIAGSADS 147
Db 121 KKAKEKIEKKGKKEKKQQSIAGSADS 147
RESULT 10
ABB59210
ID ABB59210 standard; protein; 294 AA.
XX
AC ABB59210;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 4422.
XX
KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL03313.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
PT
XX
PS Disclosure; SEQ ID NO 4422; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 294 AA;
Query Match 42.7%; Score 671; DB 4; Length 294;
Best Local Similarity 44.9%; Pred. No. 8.2e-53;
Matches 141; Conservative 57; Mismatches 88; Indels 28; Gaps 5;
QY 6 AVLKRLEQKGAADQIIIEYLKQVSLLEKAILQATLREEKKLRVENAKLKEIEELKQE 65
Db 2 ADLQQIASNNERAEALINSIEAIEISGIIQ----QLVERQKQELIKENAALAKEVEAALAQ 57
QY 66 LIQAEIQNGVKQIAFP-----SGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTG 118
Db 58 LVQLELRNGKKQIPVPGARGFCTSAAPV-----VMPAEAGPATAAPAPA----- 102
QY 119 DEKKAKEKIEKKGKKEKKQQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEE 178

Db 103 -PKPAKEPEKKSKEKKPAAEKPA-AAPEAPVDVGRLLDRVGKIVEGRHPDADSLYLEK 160
QY 179 VDVGEIAPRTVVGSLVNHVPLEQMQRNVILLCNLKPAKMRGVLSQAMVMCASSPEKIEI 238
Db 161 IDCGEAAPRTVVGSLVKFVPLEEMQNRLLVVMCNLKPAKMRGVTSQAMVMCASTPEKVEV 220
QY 239 LAPPNGSVPGDRITFDAPFGEPEKELNPKKKIWEQIQPDLHTNDECVAATYKGVFVEVKGK 298
Db 221 LSPPAGAVPGDLVHCEGYPRQPDQALNPKKIFESCAPDLKTNGELVACYKGAALHVP GK 280
QY 299 GVCRAQTMSNSGIK 312
Db 281 GNVVAQTLKNNVVK 294

RESULT 11
ABM74361
ID ABM74361 standard; protein; 280 AA.
XX
AC ABM74361;
XX
DT 17-OCT-2003 (first entry)
XX
DE DNA clone originating in barley containing SNP sequence #771.
XX
DE DNA clone originating in barley containing SNP sequence #771.
KW Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
XX
OS Hordeum vulgare.
XX
PN WO2003057877-A1.
XX
PD 17-JUL-2003.
XX
PF 16-DEC-2002; 2002WO-IB005403.
XX
PR 20-DEC-2001; 2001JP-00387059.
PR 20-DEC-2001; 2001JP-00387131.
PR 20-DEC-2001; 2001JP-00403299.
PR 20-DEC-2001; 2001JP-00403300.
PR 27-SEP-2002; 2002JP-00327515.
XX
PA (UYNI-) UNIV JAPAN OKAYAMA.
XX
PI Sato K, Takeda K, Kohara Y;
XX
DR WPI; 2003-587127/55.

XX Single nucleotide polymorphism sites in barley varieties and DNA
PT sequences containing them for analysis and identification of barley
PT varieties and production of barley transformants with desired
PT characteristics.
XX
PS Disclosure; SEQ ID XX; 284pp; Japanese.
XX
CC The present invention relates to oligonucleotide clones originating in
CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms
CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley
CC varieties, identification of particular varieties and genotype-phenotype
CC analysis, isolation of specific genes and creation of new varieties by
CC transformation of barley varieties with them and production of new barley
CC varieties with desired properties. The present sequence represents an
CC oligonucleotide clone sequence featured in the specification. The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published-pct-sequences
XX
SQ Sequence 280 AA;

Query Match 33.2%; Score 522.5; DB 7; Length 280;
Best Local Similarity 45.4%; Pred. No. 3.2e-39;
Matches 108; Conservative 42; Mismatches 77; Indels 11; Gaps 5;
QY 83 GTPLHANSMVSENVIQSTAVTTVSSGTKEQIKG-GTGDEKKAKEIKKGEK-----KEK 136

Db 46 GKPVPLEFKELKDQEEVEAFRIKFAQSQAERILKQADAEAKKVAEKL--KGTKLSESSKK 103
QY 137 KQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEDVGEIAPRTVVGSLVNH 196
Db 104 KQSGGSKSTSEDSVAKLDIRVGLIRKAEKHPDADSLYVEEDVVEEAPRTVVGSLVKF 163
QY 197 VPLEQMQRNVILLCNLKPAKMRGVLSQAMVMCASSPE--KIEILAPPNGSVPGDRITFD 254
Db 164 IPLEEMQNRKVCVLCNLKPAMRGTKSHAMVLAASNEDHTKVELVEPPESAAGERVTF 223
QY 255 APFGEPEKELNPKKKIWEQIQPDLHTNDECVAATYKGVFVEVKGVCRAQTMSNSGIK 312
Db 224 GFSGEPEASLNKSKTWEKLSADLHNGELVACYKDVFPFTTSA-GVCKVKTIANGAIR 280

RESULT 12
ABM73655
ID ABM73655 standard; protein; 289 AA.
XX
AC ABM73655;
XX
DT 17-OCT-2003 (first entry)
XX
DE DNA clone originating in barley containing SNP sequence #65.
XX
DE DNA clone originating in barley containing SNP sequence #65.
KW Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
XX
OS Hordeum vulgare.
XX
PN WO2003057877-A1.
XX
PD 17-JUL-2003.
XX
PF 16-DEC-2002; 2002WO-IB005403.
XX
PR 20-DEC-2001; 2001JP-00387059.
PR 20-DEC-2001; 2001JP-00387131.
PR 20-DEC-2001; 2001JP-00403299.
PR 20-DEC-2001; 2001JP-00403300.
PR 27-SEP-2002; 2002JP-00327515.
XX
PA (UYNI-) UNIV JAPAN OKAYAMA.
XX
PI Sato K, Takeda K, Kohara Y;
XX
DR WPI; 2003-587127/55.

XX Single nucleotide polymorphism sites in barley varieties and DNA
PT sequences containing them for analysis and identification of barley
PT varieties and production of barley transformants with desired
PT characteristics.
XX
PS Disclosure; SEQ ID XX; 284pp; Japanese.
XX
CC The present invention relates to oligonucleotide clones originating in
CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms
CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley
CC varieties, identification of particular varieties and genotype-phenotype
CC analysis, isolation of specific genes and creation of new varieties by
CC transformation of barley varieties with them and production of new barley
CC varieties with desired properties. The present sequence represents an
CC oligonucleotide clone sequence featured in the specification. The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published-pct-sequences
XX
SQ Sequence 289 AA;

Query Match 33.2%; Score 522.5; DB 7; Length 289;
Best Local Similarity 45.4%; Pred. No. 3.4e-39;
Matches 108; Conservative 42; Mismatches 77; Indels 11; Gaps 5;

Qy	83	GTPLHANSWVSENV	IQSTAVTTVSSGTKEQIKG-GTGBDEKKAKAKIEKKGEK-----KEK	136
Db	55	GKPVPLFKELKDQ	VEAFRIKFAQSQAERILKGQADAEAKKVAEKL--KGTKLSEGSKK	112
Qy	137	KQOSIAGSADSKP	IDVSRDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVVSGLVNH	196
Db	113	KQSGSKSKTSED	VSVAKLDIRVGLIRKAEKHPDADSLYVEEIDVVEEAPRTVVVSGLVKF	172
Qy	197	VPLEQMQRNVILL	CNLKPKAKMRGVLSQLMVMCASSPE--KIEILAPPNGSVPGDRITFD	254
Db	173	IPLEEMQRNKVC	VLNLKPKVAMRGIKSHAMVLAASNEDHTKVELVEPPESAAGVERTFA	232
Qy	255	AFPGEPDKELNP	KKKIWEQIQPLDHTNDECVATYKGPPEVKGKGVCRQAOTMSNGIK	312
Db	233	GFSGEPEASINAK	SKTWEKLSADLHSGNELVACYKDVPFTTSA-GVCKVKTTIANGAIR	289

RESULT 13
ABU10451
ID ABU10451 standard; protein; 108 AA.
XX
AC ABU10451;
DT
XX
XX 01-AUG-2003 (first entry)
DE Immunological enhancement agent p43 (1-108).
XX
KW Immunostimulant; cytokine agonist; p43; cytokine; interleukin-8; TNF;
KW tumour necrosis factor.
XX
XX
OS Mammalia.
XX
PN US2003004309-A1.

RESULT 14
AAE19811
ID AAE19811 standard; protein; 659 AA.
XX
AC AAE19811;
XX
DT 18-JUN-2002 (first entry)
XX
NM Com p0128 crjfbk48r clone methionyl-tRNA synthetase (MTS).

XX Corn; methionine metabolic enzyme; methionyl-tRNA synthetase; MTS;
KW methionyl-tRNA formyltransferase; MTF; transgenic plant; gene mapping;
KW plant breeding; allele specific ligation; radiation hybrid mapping;
KW nucleotide extension reaction; allele-specific amplification; enzyme;
KW physical mapping; protein; EC 6.1.1.10.

XX	OS	Zea mays.
XX	PN	US6346403-B1.
XX	PD	12-FEB-2002.
XX	PF	07-SEP-1999; 99US-00392772.
XX	PR	08-SEP-1998; 98US-0099519P.
XX	PA	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	PI	Rafalski JA, Famodu LO;
XX	DR	WPI; 2002-224991/28.
XX	DR	N-PSDB; AAD31528.
XX	PT	New isolated polynucleotide encoding plant methionyl-tRNA
XX	PT	formyltransferase or methionyl-tRNA synthetase polypeptide, useful for
XX	PT	producing transgenic plants and as probes or primers.
XX	PS	Claim 1; Col 37-40; 24pp; English.

The invention relates to nucleic acids encoding methionine metabolic enzymes, methionyl-tRNA formyltransferase (MTF) and methionyl-tRNA synthetase (MTS). The nucleic acids of the invention are useful for selecting an isolated polynucleotide that affects the level of expression of MTS or MTF polypeptide in a cell. They are useful as a probe or primer for obtaining a nucleic acid fragment encoding a substantial portion of MTF or MTS, preferably plant MTF or plant MTS gene. They are also useful for creating transgenic plants in which the MTS or MTF polypeptides are present at higher or lower levels than normal or in cell types or in developmental stages in which they are not normally found. These sequences may also be used as probes for genetically and physically mapping the genes that they are a part of and used as markers for traits linked to those genes. This information is used in plant breeding in order to develop lines with desired phenotypes. These sequences are also used in a variety of amplification based methods of genetic and physical mapping such as allele-specific amplification, polymorphism of PCR amplified fragments, allele specific ligation, nucleotide extension reactions and radiation hybrid mapping. The present sequence is corn MTS enzyme

[illegible]

Db 430 LKDE-----DVALHREKYAGSQAERSSKAAADAANKVANQLKG---- 468

QY 120 EKKAKEKIEKKGEKKKQSQIAGSADSK-----PIDVSRDLRIGCIITARKHPDADSLY 175

Db 469 -----TKLSDGGTKKEPKQS--GGSKSKTAEADITVAKLDIRVGLIRKAHKHPDADSLY 521

QY 176 VEEVDVGEIAPRTVVSGLVNHVPLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPE- 234

Db 522 VEEIDVGEDAPRTVVSGLVKFIPLEEMQSRKVCVLCNLKPVAMRGIKSHAMVLAASNEHDH 581

QY 235 -KIEILAPPNGSVPGDRITFDAFPGEPPDKELNPKKKIWEQIQPDLHTNDEC VATYKGVPF 293

Db 582 TKVELVEPPESAAGGERVTFAGYAGEPEASLSGKSKTWEKLAELHSHNGELVACYRDVPF 641

QY 294 EVKGGVCVCAQTMSNSGIK 312

Db 642 TTSA-GVCRVKTIANGEIR 659

RESULT 15

ADN99968

ID ADN99968 standard; protein; 95 AA.

XX

AC ADN99968;

XX

DT 29-JUL-2004 (first entry)

XX

DE Novel human protein sequence #784.

XX

KW anti-inflammatory; dermatological; neuroprotective; immunomodulator;

KW antibacterial; virucide; antipsoriatic; cytostatic; gene therapy;

KW vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes;

KW early aging; hormonal imbalance; ischemic heart disease;

KW ulcerative colitis.

XX

OS Homo sapiens.

XX

PN WO2004038003-A2.

XX

PD 06-MAY-2004.

XX

PF 24-OCT-2003; 2003WO-US033947.

XX

PR 25-OCT-2002; 2002US-0421061P.

PR 25-OCT-2002; 2002US-0421080P.

PR 25-OCT-2002; 2002US-0421552P.

PR 25-OCT-2002; 2002US-0421614P.

PR 30-OCT-2002; 2002US-0422177P.

PR 30-OCT-2002; 2002US-0422178P.

PR 15-NOV-2002; 2002US-0426355P.

PR 15-NOV-2002; 2002US-0426384P.

PR 15-NOV-2002; 2002US-0426394P.

PR 15-NOV-2002; 2002US-0426430P.

PR 15-NOV-2002; 2002US-0426916P.

PR 27-NOV-2002; 2002US-0429224P.

PR 27-NOV-2002; 2002US-0429275P.

PR 27-NOV-2002; 2002US-0429302P.

PR 27-NOV-2002; 2002US-0429326P.

PR 27-NOV-2002; 2002US-0429651P.

PR 04-DEC-2002; 2002US-0430645P.

PR 04-DEC-2002; 2002US-0430651P.

PR 04-DEC-2002; 2002US-0430657P.

PR 04-DEC-2002; 2002US-0430663P.

PR 04-DEC-2002; 2002US-0430668P.

PR 04-DEC-2002; 2002US-0430684P.

PR 05-DEC-2002; 2002US-0430937P.

PR 05-DEC-2002; 2002US-0430965P.

PR 05-DEC-2002; 2002US-0431458P.

PR 12-DEC-2002; 2002US-0433251P.

PR 12-DEC-2002; 2002US-0433500P.

PR 13-DEC-2002; 2002US-0433316P.

PR 13-DEC-2002; 2002US-0433318P.

PR 23-DEC-2002; 2002US-0436236P.

PR 03-JAN-2003; 2003US-0437914P.

PR 17-JAN-2003; 2003US-0440820P.

PR 17-JAN-2003; 2003US-0440821P.

PR 18-APR-2003; 2003US-0463700P.

PR 18-APR-2003; 2003US-0463708P.

PR 18-APR-2003; 2003US-0463716P.

PR 18-APR-2003; 2003US-0463732P.

PR 02-MAY-2003; 2003US-0467199P.

PR 02-MAY-2003; 2003US-0467201P.

PR 02-MAY-2003; 2003US-0467203P.

PR 02-MAY-2003; 2003US-0467230P.

PR 19-MAY-2003; 2003US-0471306P.

PR 19-MAY-2003; 2003US-0471336P.

PR 22-MAY-2003; 2003US-0472420P.

PR 22-MAY-2003; 2003US-0472430P.

PR 09-JUN-2003; 2003US-0476609P.

PR 09-JUN-2003; 2003US-0476621P.

PR 09-JUN-2003; 2003US-0476632P.

PR 09-JUN-2003; 2003US-0476641P.

PR 08-JUL-2003; 2003US-0485217P.

PR 08-JUL-2003; 2003US-0485218P.

PR 08-JUL-2003; 2003US-0485223P.

PR 08-JUL-2003; 2003US-0485224P.

PR 08-JUL-2003; 2003US-0485325P.

PR 08-JUL-2003; 2003US-0485359P.

PR 14-JUL-2003; 2003US-0486446P.

PR 14-JUL-2003; 2003US-0486480P.

PR 15-JUL-2003; 2003US-0486891P.

PR 15-JUL-2003; 2003US-0486960P.

PR 08-AUG-2003; 2003US-0493341P.

PR 08-AUG-2003; 2003US-0493370P.

PR 08-AUG-2003; 2003US-0493573P.

PR 08-AUG-2003; 2003US-0493577P.

XX

XX (FIVE-) FIVE PRIME THERAPEUTICS INC.

PA

XX

PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;

PI Halenbeck RF, Kothakota S, Lin H, Linnemann T, Pierce K, wang Y;

PI Wong JGP, Wu G, Zhang H, zeng C;

XX

DR WPI; 2004-365511/34.

DR N-PSDB; ADN99184.

XX

PT New nucleic acid molecules, useful in preparing a composition for

PT treating or preventing e.g. inflammatory, CNS, bacterial or viral

PT disorders, cancer, psoriasis, diabetes, ischemic heart disease or

PT ulcerative colitis.

XX

PS Claim 14; SEQ ID NO 1568; 532pp; English.

XX

CC The invention relates to a nucleic acid molecule comprising a

CC polynucleotide sequence or its complement that encodes a polypeptide. The

CC nucleic acid is useful in preparing a composition for treating or

CC preventing inflammatory, CNS, immune, bacterial or viral disorder,

CC cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic

CC heart disease or ulcerative colitis. This sequence corresponds to a

CC protein of the invention.

XX

SQ Sequence 95 AA;

Query Match 32.2%; Score 507; DB 8; Length 95;

Best Local Similarity 100.0%; Pred. No. 1.8e-38;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 MRGVLSQLAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPPDKELNPKKKIWEQIQPD 277

Db 1 MRGVLSQLAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPPDKELNPKKKIWEQIQPD 60

QY 278 LHTNDEC VATYKGVPFVKGKVCRAQTMSNSGIK 312

Db 61 LHTNDEC VATYKGVPFVKGKVCRAQTMSNSGIK 95

Search completed: January 14, 2005, 15:55:12
Job time : 163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2005, 15:49:58 ; Search time 40 Seconds
(without alignments)
517.280 Million cell updates/sec

Title: US-09-733-306C-4
Perfect score: 1573
Sequence: 1 MANNDVILKRLKLEQKGAEDQ.....FEVKGKVCRAQTMSNSGIK 312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1568	99.7	312	3	US-08-360-821B-36 Sequence 36, Appl
2	1568	99.7	312	4	US-09-851-026-36 Sequence 36, Appl
3	1510	96.0	310	1	US-08-129-456A-37 Sequence 37, Appl
4	1343	85.4	310	1	US-08-129-456A-36 Sequence 36, Appl
5	1343	85.4	310	2	US-08-705-868-3 Sequence 3, Appli
6	1343	85.4	310	3	US-09-123-615-3 Sequence 3, Appli
7	1343	85.4	310	3	US-08-360-821B-35 Sequence 35, Appl
8	1343	85.4	310	4	US-09-851-026-35 Sequence 35, Appl
9	931	59.2	183	3	US-08-483-534A-7 Sequence 7, Appli
10	835	53.1	166	1	US-08-129-456A-11 Sequence 11, Appl
11	835	53.1	166	3	US-08-360-821B-11 Sequence 11, Appl
12	835	53.1	166	4	US-09-851-026-11 Sequence 11, Appl
13	510.5	32.5	659	3	US-09-392-772-10 Sequence 10, Appl
14	440.5	28.0	301	2	US-08-705-868-1 Sequence 1, Appli
15	440.5	28.0	301	3	US-09-123-615-1 Sequence 1, Appli
16	440.5	28.0	301	4	US-09-919-039-132 Sequence 132, App
17	438.5	27.9	215	4	US-09-248-796A-19812 Sequence 19812, A
18	429.5	27.3	168	3	US-08-483-534A-2 Sequence 2, Appli
19	235	14.9	174	4	US-09-248-796A-19813 Sequence 19813, A
20	227	14.4	720	4	US-09-328-352-4765 Sequence 4765, Ap
21	188.5	12.0	674	4	US-09-107-532A-6201 Sequence 6201, Ap
22	186.5	11.9	648	1	US-08-451-715A-4 Sequence 4, Appli
23	182.5	11.6	111	4	US-09-489-039A-9293 Sequence 9293, Ap
24	174.5	11.1	493	4	US-09-134-000C-4034 Sequence 4034, Ap
25	157	10.0	665	3	US-08-844-059-2 Sequence 2, Appli
26	157	10.0	665	3	US-09-431-202-2 Sequence 2, Appli
27	152.5	9.7	679	4	US-09-583-110-2751 Sequence 2751, Ap

28	147	9.3	221	4	US-09-252-991A-21654	Sequence 21654, A
29	136	8.6	716	4	US-09-489-039A-8243	Sequence 8243, Ap
30	134.5	8.6	680	4	US-09-252-991A-17566	Sequence 17566, A
31	129	8.2	690	4	US-09-540-236-3507	Sequence 3507, Ap
32	128	8.1	115	3	US-08-844-059-4	Sequence 4, Appli
33	128	8.1	115	3	US-09-431-202-4	Sequence 4, Appli
34	128	8.1	683	4	US-09-543-681A-5403	Sequence 5403, Ap
35	119.5	7.6	589	4	US-09-543-681A-7643	Sequence 7643, Ap
36	117	7.4	721	3	US-09-134-078-19	Sequence 19, Appl
37	116.5	7.4	414	5	PCT-US93-03077-3	Sequence 3, Appli
38	116.5	7.4	1093	5	PCT-US93-03077-1	Sequence 1, Appli
39	115.5	7.3	1493	4	US-09-713-273A-20	Sequence 20, Appl
40	115	7.3	890	4	US-09-849-602-19	Sequence 19, Appl
41	114.5	7.3	271	1	US-08-664-596B-11	Sequence 11, Appl
42	114.5	7.3	431	4	US-09-286-981B-3	Sequence 3, Appli
43	113.5	7.2	618	4	US-09-710-279-860	Sequence 860, App
44	113.5	7.2	660	3	US-09-134-001C-3350	Sequence 3350, Ap
45	113	7.2	127	4	US-09-543-681A-7844	Sequence 7844, Ap

ALIGNMENTS

RESULT 1
US-08-360-821B-36
; Sequence 36, Application US/08360821B
; Patent No. 6228837
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Clauss, Matthias
; APPLICANT: Kao, Janet
; APPLICANT: Kayton, Mark
; APPLICANT: Libutti, Steven K
; TITLE OF INVENTION: Endothelial Monocyte Activating
; TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821B
; FILING DATE: 08-OCT-96
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-360-821B-36

Query Match 99.7%; Score 1568; DB 3; Length 312;
Best Local Similarity 99.7%; Pred. No. 2.7e-136;
Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MANNDVILKRLKLEQKGAEDQIIIEYLKQVSLKKEKAILQATLREEKLRVENAKLKEIE 60

Query Match 99.7%; Score 1568; DB 4; Length 312;
Best Local Similarity 99.7%; Pred.No.2.7e-136;
Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MANNDVLRLEQKGAADQIIIEYLKQOVSLLEKAILQATLREEKKLRVENAKLKKEIE 60
Db 1 MANNDVLRLEQKGAADQIIIEYLKQOVSLLEKAILQATLREEKKLRVENAKLKKEIE 60

QY 61 ELKQELIQAEIQNGVKQIAFPSPGTPLHANSMVSENVIOSTAVTTVSSSGTKEQIKGGTGDE 120
Db 61 ELKQELIQAEIQNGVKQIPFPSPGTPLHANSMVSENVIOSTAVTTVSSSGTKEQIKGGTGDE 120

QY 121 KKAKEKIEKKGEKKKQOQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 180
Db 121 KKAKEKIEKKGEKKKQOQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 180

QY 181 VGEIAPRTVVSLVNHVPLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
Db 181 VGEIAPRTVVSLVNHVPLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240

QY 241 PPNGSVPGDRITFDAPGPEPDKELNPKKKIWEQIQPDLHTNDECVAATYKGVPEVKGKGV 300
Db 241 PPNGSVPGDRITFDAPGPEPDKELNPKKKIWEQIQPDLHTNDECVAATYKGVPEVKGKGV 300

QY 301 CRAFTMSNSGK 312
Db 301 CRAFTMSNSGK 312

RESULT 3
US-08-129-456A-37
; Sequence 37, Application US/08129456A
; Patent No. 5641867
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Clauss, Matthias
; APPLICANT: Kao, Janet
; APPLICANT: Kayton, Mark
; APPLICANT: Libutti, Steven K.
; TITLE OF INVENTION: Endothelial-Monocyte Activating
; TITLE OF INVENTION: Polypeptide II: A Mediator Which
; TITLE OF INVENTION: Activates Host Response
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0 Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,456A
; FILING DATE: 29-SEP-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 278 0400
; TELEFAX: 212 391 0526
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-129-456A-37

Db 1 MANNDVLRLEQKGAADQIIIEYLKQOVSLLEKAILQATLREEKKLRVENAKLKKEIE 60
QY 61 ELKQELIQAEIQNGVKQIAFPSPGTPLHANSMVSENVIOSTAVTTVSSSGTKEQIKGGTGDE 120
Db 61 ELKQELIQAEIQNGVKQIPFPSPGTPLHANSMVSENVIOSTAVTTVSSSGTKEQIKGGTGDE 120

QY 121 KKAKEKIEKKGEKKKQOQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 180
Db 121 KKAKEKIEKKGEKKKQOQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 180

QY 181 VGEIAPRTVVSLVNHVPLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
Db 181 VGEIAPRTVVSLVNHVPLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240

QY 241 PPNGSVPGDRITFDAPGPEPDKELNPKKKIWEQIQPDLHTNDECVAATYKGVPEVKGKGV 300
Db 241 PPNGSVPGDRITFDAPGPEPDKELNPKKKIWEQIQPDLHTNDECVAATYKGVPEVKGKGV 300

QY 301 CRAFTMSNSGK 312
Db 301 CRAFTMSNSGK 312

RESULT 2
US-09-851-026-36
; Sequence 36, Application US/09851026
; Patent No. 6734168
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Clauss, Matthias
; APPLICANT: Kao, Janet
; APPLICANT: Kayton, Mark
; APPLICANT: Libutti, Steven K.
; TITLE OF INVENTION: Endothelial Monocyte Activating
; TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,026
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821
; FILING DATE: 08-OCT-96
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
; US-09-851-026-36

Query Match 96.0%; Score 1510; DB 1; Length 310;
Best Local Similarity 97.8%; Pred. No. 5.9e-131;
Matches 306; Conservative 0; Mismatches 3; Indels 4; Gaps 3;

QY 1 MANNDVLRLEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKKEIE 60
|||
Db 1 MANNDVLRLEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKKEIE 60
|||

QY 61 ELKQELIQAEIQNGVKQIAFPSPGTPHLHANSMVSENVIOSTAV-TTVSSGTKEQIKGGTGD 119
|||
Db 61 ELKQELIQAEIQNGVKQIPFPSPGTPHLHANSMVSENVIOSTAVATTVSSGTKEQIK--AGD 118
|||

QY 120 EKKAKEIEKKGEKKEKKQOSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEV 179
|||
Db 119 EKKAKEIEKKGEKK-KKQOSIAGSADSKPIDASRLDLRIGCIITARKHPDADSLYVEEV 177
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QY 180 DVGEIAPRTVVSGLVNHVPLEQMQRNVILLCNLKPAKMRGVLVSQAMVMCASSPEKIEIL 239
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Db 178 DVGEIAPRTVVSGLVNHVPLEQMQRNVILLCNLKPAKMRGVLVSQAMVMCASSPEKIEIL 237
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QY 240 APPNGSVPGDRITFDAPFGPEPKELNPKKKEIWEQIQPDLHTNDEC VATYKGVPPFEVKGKG 299
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Db 238 APPNGSVPGDRITFDAPFGPEPKELNPKKKEIWEQIQPDLHTNDEC VATYKGVPPFEVKGKG 297
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QY 300 VCRAQTMSNSGIK 312
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Db 298 VCRAQTMSNSGIK 310
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RESULT 4
US-08-129-456A-36
; Sequence 36, Application US/08129456A
; Patent No. 5641867
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Clauss, Matthias
; APPLICANT: Kao, Janet
; APPLICANT: Kayton, Mark
; APPLICANT: Libutti, Steven K.
; TITLE OF INVENTION: Endothelial-Monocyte Activating
; TITLE OF INVENTION: Polypeptide II: A Mediator Which
; TITLE OF INVENTION: Activates Host Response
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0 Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,456A
; FILING DATE: 29-SEP-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 278 0400
; TELEFAX: 212 391 0526
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-129-456A-36
Query Match 85.4%; Score 1343; DB 1; Length 310;
Best Local Similarity 85.9%; Pred. No. 1.4e-115;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;

QY 1 MANNDVLRLEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKKEIE 60
|||
Db 1 MATNDVLRLEQKGAADQIIIEYLKQVALLKEKAILQATMREKKLRVENAKLKKEIE 60
|||

QY 61 ELKQELIQAEIQNGVKQIAFPSPGTPHLHANSMVSENVIOSTAV-TTVSSGTKEQIKGGTGD 119
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Db 61 ELKQELILAEIHNGVEQVRVRLSTPLQTNCTASESVVQSPSVATTASPATKEQIK--AGE 118
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QY 120 EKKAKEIEKKGEKKEKKQOSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEV 179
|||
Db 119 EKKVKEKTEKKGEKKE-KQOSAAASTDSKPIDASRLDLRIGCIITAKKHPDADSLYVEEV 177
|||

QY 180 DVGEIAPRTVVSGLVNHVPLEQMQRNVILLCNLKPAKMRGVLVSQAMVMCASSPEKIEIL 239
|||
Db 178 DVGEAAPRTVVSGLVNHVPLEQMQRNVILLCNLKPAKMRGVLVSQAMVMCASSPEKVEIL 237
|||

QY 240 APPNGSVPGDRITFDAPFGPEPKELNPKKKEIWEQIQPDLHTNDEC VATYKGVPPFEVKGKG 299
|||
Db 238 APPNGSVPGDRITFDAPFGPEPKELNPKKKEIWEQIQPDLHTNAECVATYKGAPFEVKGKG 297
|||

QY 300 VCRAQTMSNSGIK 312
|||
Db 298 VCRAQTMSNSGIK 310
|||

RESULT 5
US-08-705-868-3
; Sequence 3, Application US/08705868
; Patent No. 5885798
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,868
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0117 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank

CLONE: 498910
US-08-705-868-3
Query Match 85.4%; Score 1343; DB 2; Length 310;
Best Local Similarity 85.9%; Pred. No. 1.4e-115;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;
QY 1 MANNDAVLKRLKQKGAADQIIIEYKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60
Db 1 MATNDAVLKRLKQKGAADQIIIEYKQOVALLKEKAILQATMREKKLRVENAKLKEIE 60
QY 61 ELKQELIQAEIQNGVKQIAFPSTGTPHANSVMVSENVIOSTAV-TTVSSGTKEQIKGGTGD 119
Db 61 ELKQELILAEIHNGVEQVRVRLSTPLQTNCTASESVVQSPSVATTASPATKEQIK--AGE 118
QY 120 EKKAKEKIEKKGEKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEV 179
Db 119 EKKVKEKTEKKGEKKE-KQOSAAASTDSKPIDASRLDLRIGCIIVTAKKHPDADSLYVEEV 177
QY 180 DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEIL 239
Db 178 DVGEAAPRTVVSGLVNHVPLEQMQNRMVVLLCNLKPAMRGVLSQAMVMCASSPEKVEIL 237
QY 240 APPNGSVPGDRITFDAPPGEKELNPKKKIWEQIQPDLHTNDECVATYKGVPEVKGK 299
Db 238 APPNGSVPGDRITFDAPPGEKELNPKKKIWEQIQPDLHTNAECVATYKGAPFEVKGK 297
QY 300 VCRAQTMSNSGIK 312
Db 298 VCRAQTMANSIGIK 310

RESULT 6
US-09-123-615-3
Sequence 3, Application US/09123615
Patent No. 6090377
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
APPLICANT: Au-Young, Janice
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,615
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,868
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0117 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 498910
US-09-123-615-3
Query Match 85.4%; Score 1343; DB 3; Length 310;
Best Local Similarity 85.9%; Pred. No. 1.4e-115;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;
QY 1 MANNDAVLKRLKQKGAADQIIIEYKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60
Db 1 MATNDAVLKRLKQKGAADQIIIEYKQOVALLKEKAILQATMREKKLRVENAKLKEIE 60
QY 61 ELKQELIQAEIQNGVKQIAFPSTGTPHANSVMVSENVIOSTAV-TTVSSGTKEQIKGGTGD 119
Db 61 ELKQELILAEIHNGVEQVRVRLSTPLQTNCTASESVVQSPSVATTASPATKEQIK--AGE 118
QY 120 EKKAKEKIEKKGEKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEV 179
Db 119 EKKVKEKTEKKGEKKE-KQOSAAASTDSKPIDASRLDLRIGCIIVTAKKHPDADSLYVEEV 177
QY 180 DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEIL 239
Db 178 DVGEAAPRTVVSGLVNHVPLEQMQNRMVVLLCNLKPAMRGVLSQAMVMCASSPEKVEIL 237
QY 240 APPNGSVPGDRITFDAPPGEKELNPKKKIWEQIQPDLHTNDECVATYKGVPEVKGK 299
Db 238 APPNGSVPGDRITFDAPPGEKELNPKKKIWEQIQPDLHTNAECVATYKGAPFEVKGK 297
QY 300 VCRAQTMSNSGIK 312
Db 298 VCRAQTMANSIGIK 310

RESULT 7
US-08-360-821B-35
Sequence 35, Application US/08360821B
Patent No. 6228837
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Clauss, Matthias
APPLICANT: Kao, Janet
APPLICANT: Kayton, Mark
APPLICANT: Libutti, Steven K.
TITLE OF INVENTION: Endothelial Monocyte Activating Polypeptide II: A Mediator Which Activates Host Response
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,821B
FILING DATE: 08-OCT-96
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 35:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-360-821B-35

Query Match      85.4%; Score 1343; DB 3; Length 310;
Best Local Similarity 85.9%; Pred. No. 1.4e-115;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;

QY 1 MANNDVAVLKRLEQKGAEADQIIIEYLKQQVSLKKEKAILQATLREEKKLRVENAKLKKEIE 60
Db 1 MATNDVAVLKRLEQKGAEADQIIIEYLKQQVALLKEKAILQATMREEKKLRVENAKLKKEIE 60
QY 61 ELKQELIQAEIQNGVKQIAPPSGTPLHANSVMSENVIOSTAV-TTVSSGTYKEQIKGGTGD 119
Db 61 ELKQELILAEIHNGVEQVRVRLSTPLQTNCTASESVVQSPSVATTASPATKEQIK--AGE 118
QY 120 EKKAKEKIEKKEKKEKQSIAGSADSKPIDVSRDLRLRIGCIITARKHPDADSLYVEEV 179
Db 119 EKKVKEKTEKKEKKE-KQSSAAASTDSKPIDASRLDLRIGCIVTAKKHPDADSLYVEEV 177
QY 180 DVGEIAPRTVVSGLVNHVPLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPEKIEIL 239
Db 178 DVGEAAPRTVVSGLVNHVPLEQMQRNVLLCNLKPAMRGVLSQAMVMCASSPEKVEIL 237
QY 240 APPNGSVPGDRITFDAPPGEKPKELNPKKKIWEIQPDHLTNDCECVATYKGVFFVKGKG 299
Db 238 APPNGSVPGDRITFDAPPGEKPKELNPKKKIWEIQPDHLTNAECVATYKGAPFEVKGKG 297
QY 300 VCRAQTMNSNGIK 312
Db 298 VCRAQTMANSNGIK 310

RESULT 8
US-09-851-026-35
; Sequence 35, Application US/09851026
; Patent No. 6734168
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; Clauss, Matthias
; Kao, Janet
; Kayton, Mark
; Libutti, Steven K
; TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,026
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821
; FILING DATE: 08-OCT-96
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-851-026-35

Query Match      85.4%; Score 1343; DB 4; Length 310;
Best Local Similarity 85.9%; Pred. No. 1.4e-115;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;

QY 1 MANNDVAVLKRLEQKGAEADQIIIEYLKQQVSLKKEKAILQATLREEKKLRVENAKLKKEIE 60
Db 1 MATNDVAVLKRLEQKGAEADQIIIEYLKQQVALLKEKAILQATMREEKKLRVENAKLKKEIE 60
QY 61 ELKQELIQAEIQNGVKQIAPPSGTPLHANSVMSENVIOSTAV-TTVSSGTYKEQIKGGTGD 119
Db 61 ELKQELILAEIHNGVEQVRVRLSTPLQTNCTASESVVQSPSVATTASPATKEQIK--AGE 118
QY 120 EKKAKEKIEKKEKKEKQSIAGSADSKPIDVSRDLRLRIGCIITARKHPDADSLYVEEV 179
Db 119 EKKVKEKTEKKEKKE-KQSSAAASTDSKPIDASRLDLRIGCIVTAKKHPDADSLYVEEV 177
QY 180 DVGEIAPRTVVSGLVNHVPLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPEKIEIL 239
Db 178 DVGEAAPRTVVSGLVNHVPLEQMQRNVLLCNLKPAMRGVLSQAMVMCASSPEKVEIL 237
QY 240 APPNGSVPGDRITFDAPPGEKPKELNPKKKIWEIQPDHLTNDCECVATYKGVFFVKGKG 299
Db 238 APPNGSVPGDRITFDAPPGEKPKELNPKKKIWEIQPDHLTNAECVATYKGAPFEVKGKG 297
QY 300 VCRAQTMNSNGIK 312
Db 298 VCRAQTMANSNGIK 310

RESULT 9
US-08-483-534A-7
; Sequence 7, Application US/08483534A
; Patent No. 6013483
; GENERAL INFORMATION:
; APPLICANT: Coleman, Timothy A
; APPLICANT: Rosen, Craig
; TITLE OF INVENTION: Endothelial-Monocyte Activating
; TITLE OF INVENTION: Polypeptide III
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,534A
; FILING DATE: 07 JUN 95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-464 (PF206)

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-483-534A-7

Query Match 59.2%; Score 931; DB 3; Length 183;
Best Local Similarity 98.4%; Pred. No. 6e-78;
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 130 KGEKKEKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTV 189
Db 1 KGEKKEKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTV 60

QY 190 VSGLNVHVPLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPEKIEILLAPPNGSVPGD 249
Db 61 VSGLNVHVPLEQMQRNVILLCNLKPAMRGVKSQAMVMCASSPEKIEILLAPPNGSVPGD 120

QY 250 RITFDAPGPEPKELNPKKIWEIQPDLHTNDEC VATYKGVPFVKGKVCRAQTMSNS 309
Db 121 RITFDAPGPEPKELNPKKIWEIQPDLHTNDEC VATYKEVPFVKGKVCRAQTMSNS 180

QY 310 GIK 312
Db 181 GIK 183

RESULT 10
US-08-129-456A-11
; Sequence 11, Application US/08129456A
; Patent No. 5641867
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Clauss, Matthias
; APPLICANT: Kao, Janet
; APPLICANT: Kayton, Mark
; APPLICANT: Libutti, Steven K.
; TITLE OF INVENTION: Endothelial-Monocyte Activating
; TITLE OF INVENTION: Polypeptide II: A Mediator Which
; TITLE OF INVENTION: Activates Host Response
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0 Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,456A
; FILING DATE: 29-SEP-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 278 0400
; TELEFAX: 212 391 0526
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-129-456A-11

Query Match 53.1%; Score 835; DB 1; Length 166;
Best Local Similarity 94.0%; Pred. No. 3.6e-69;
Matches 156; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 147 SKPIDVSRDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLNVHVPLEQMQRNM 206
Db 1 SKPIDASRLDLRIGCIIVTAKKHPDADSLYVEEVDVGEAPRTVVSGLNVHVPLEQMQRNM 60

QY 207 VILLCNLKPAMRGVLSQAMVMCASSPEKIEILLAPPNGSVPGDRITFDAPGPEPKELNP 266
Db 61 VLLCNLKPAMRGVLSQAMVMCASSPDKVEILLAPPNGSVPGDRITFDAPGPEPKELNP 120

QY 267 KKKIWEIQPDLHTNDEC VATYKGVPFVKGKVCRAQTMSNSGIK 312
Db 121 KKKIWEIQPDLHTNAECVATYKGAPFVKGKVCRAQTMSNSGIK 166

RESULT 11
US-08-360-821B-11
; Sequence 11, Application US/08360821B
; Patent No. 6228837
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Clauss, Matthias
; APPLICANT: Kao, Janet
; APPLICANT: Kayton, Mark
; APPLICANT: Libutti, Steven K.
; TITLE OF INVENTION: Endothelial Monocyte Activating
; TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821B
; FILING DATE: 08-OCT-96
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-360-821B-11

Query Match 53.1%; Score 835; DB 3; Length 166;
Best Local Similarity 94.0%; Pred. No. 3.6e-69;
Matches 156; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 147 SKPIDVSRDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLNVHVPLEQMQRNM 206

Db 1 SKPIDASRLDLRIGCIIVTAKGHPDADSLYVEEVDVGEAAPRTVVSGLVNHHVPLEQMQRN 60

QY 207 VILLCNLKPAMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAPFGEPEKELNP 266

Db 61 VLLCNLKPAMRGVLSQAMVMCASSPKVIEILAPPNGSVPGDRITFDAPFGEPEKELNP 120

QY 267 KKKIWEIQPDLHTNDECVAITYKGVPEVKGKGVCRQAQTMNSNGIK 312

Db 121 KKKIWEIQPDLHTNAECVAITYKGAPFEVKGKGVCRQAQTMANSIGK 166

RESULT 12

US-09-851-026-11

; Sequence 11, Application US/09851026

; Patent No. 6734168

GENERAL INFORMATION:

APPLICANT: Stern, David M.

Clauss, Matthias

Kayton, Mark

Libutti, Steven K

TITLE OF INVENTION: Endothelial Monocyte Activating

Polyptide II: A Mediator Which Activates Host Response

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham, LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.30, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/851,026

FILING DATE: 07-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/360,821

FILING DATE: 08-OCT-96

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41735-A-PCT-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-851-026-11

Query Match 53.1%; Score 835; DB 4; Length 166;

Best Local Similarity 94.0%; Pred. No. 3.6e-69;

Matches 156; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 147 SKPIDASRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHHVPLEQMQRN 206

Db 1 SKPIDASRLDLRIGCIIVTAKGHPDADSLYVEEVDVGEAAPRTVVSGLVNHHVPLEQMQRN 60

QY 207 VILLCNLKPAMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAPFGEPEKELNP 266

Db 61 VLLCNLKPAMRGVLSQAMVMCASSPKVIEILAPPNGSVPGDRITFDAPFGEPEKELNP 120

QY 267 KKKIWEIQPDLHTNDECVAITYKGVPEVKGKGVCRQAQTMNSNGIK 312

Db 121 KKKIWEIQPDLHTNAECVAITYKGAPFEVKGKGVCRQAQTMANSIGK 166

RESULT 13

US-09-392-772-10

; Sequence 10, Application US/09392772

; Patent No. 6346403

GENERAL INFORMATION:

APPLICANT: Famodu, Layo O.

APPLICANT: Antoni Rafalski

TITLE OF INVENTION: Methionine Metabolic Enzymes

FILE REFERENCE: BB-1241

CURRENT APPLICATION NUMBER: US/09/392,772

CURRENT FILING DATE: 1999-09-07

EARLIER APPLICATION NUMBER: 60/099,519

EARLIER FILING DATE: 1998-09-08

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Microsoft Office 97

SEQ ID NO 10

LENGTH: 659

TYPE: PRT

ORGANISM: Zea mays

US-09-392-772-10

Query Match 32.5%; Score 510.5; DB 3; Length 659;

Best Local Similarity 38.6%; Pred. No. 2.1e-38;

Matches 123; Conservative 49; Mismatches 84; Indels 11; Gaps 11;

QY 18 ADQIIIEYLKQQVSLKKEKAILQATLREBKRLRVENAKLKE-----IEE 61

Db 380 SDEVL---RQLNLSPEENL---SLSEKG--EIAKAKTPWNFVPAGHRIGKPAPLFKE 429

QY 62 LKQELIQAEIQNGVKQIAFPSPGTPLHANSVMVSENVIQSTAVTTVSSGK--EQIKGGTGD 119

Db 430 LKDE-----DVALHREKYAGSQAERSSKAAADAENKVNQLKG---- 468

QY 120 EKKAKEKIEKKGEKKEKKQOQSIAGSADSK----PIDVSRDLRLRIGCIITARKHPDADSLY 175

Db 469 -----TKLSDGGTKKEPKQS--GGSKSKTAEADITVAKLDIRVGLIRKAEKHPDADSLY 521

QY 176 VEEVDVGEIAPRTVVSGLVNHHVPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPE- 234

Db 522 VEEIDVGEDAPRTVVSGLVKFIPLSEMQSRKVCVLCNLKPVAMRGIKSHAMVLAASNEH 581

QY 235 -KIEILAPPNGSVPGDRITFDAPFGEPEKELNPKKIWEIQPDLHTNDECVAITYKGVPE 293

Db 582 TKVELVEPPESAAGVGERVTFAGYAGEPEASLSGSKTWEKLAELHNSGELVACYRDVPF 641

QY 294 EVKKGKGVCRQAQTMNSNGIK 312

Db 642 TTSA-GVCRVKTIANGEIR 659

RESULT 14

US-08-705-868-1

; Sequence 1, Application US/08705868

; Patent No. 5885798

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Coleman, Roger

APPLICANT: Au-Young, Janice

APPLICANT: Murry, Lynn E.

TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

[illegible]

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RESULT 15
US-09-123-615-1
; Sequence 1, Application US/09123615
; Patent No. 6090377
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,615
; FILING DATE:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,868
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0117 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
;
US-09-123-615-1

Query Match      28.0%; Score 440.5; DB 3; Length 301;
Best Local Similarity 49.5%; Pred. No. 1.9e-32;
Matches 94; Conservative 36; Mismatches 51; Indels 9; Gaps 6;

QY    123 AKEKIEKKGEKKEKKQQSIA-GSA-DSKPIDV--SRDLRLRIGCIITARKHPDADSLYVEE 178
      ||:| | :||:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db    105 ALKKLASAAYPDPSKQPKMAKGPAKNSEPEEVIPSRDLIRVGKIITVEKHPPDADSLYVEK 164

QY    179 VDVGEGIAPRTVVSGLVNHHVPLEQMQRNVILLCNLKPAKMRGVLSQLAMVMCASSP---EK 235
      :||| |:||||| | | :|:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db    165 IDVGAEAPRTVVSGLVQVFVPKEELQDRLLVVVLCNLKPQMKRGVESQGMLLCASIEGINRQ 224

QY    236 IEILAPPNGSVPGDRITTFDAF-PGEPDKELNPKKKIWEIQPDLHTNDCEVATYKGVPFPE 294
      :||| | |||:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db    225 VEPLDPFPAGSAPGHVFKGYEKGQPDEELKPKKKVFEKLQADFKEISEECIAQWKQTNFM 284

QY    295 VK-GKGV CRA 303
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Db    285 TKLGSI SCKS 294

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Job time : 41 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2005, 15:52:33 ; Search time 151 Seconds
(without alignments)
746.505 Million cell updates/sec

Title: US-09-733-306C-4
Perfect score: 1573
Sequence: 1 MANNDVLRLEQKGAEADQ.....FEVKGKGVCRQTMSNSGIK 312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1568	99.7	312	9 US-09-851-026-36	Sequence 36, Appl
2	1343	85.4	310	9 US-09-851-026-35	Sequence 35, Appl
3	835	53.1	166	9 US-09-851-026-11	Sequence 11, Appl
4	831	52.8	166	10 US-09-930-169-3	Sequence 3, Appli
5	831	52.8	166	16 US-10-823-730-3	Sequence 3, Appli
6	709	45.1	147	10 US-09-930-169-1	Sequence 1, Appli
7	709	45.1	147	16 US-10-823-730-1	Sequence 1, Appli
8	528	33.6	353	15 US-10-424-599-180396	Sequence 180396,
9	517.5	32.9	377	17 US-10-425-115-350232	Sequence 350232,
10	517	32.9	804	16 US-10-437-963-183001	Sequence 2, Appli
11	516	32.8	108	10 US-09-930-169-2	Sequence 2, Appli
12	516	32.8	108	16 US-10-823-730-2	Sequence 2, Appli
13	511	32.5	792	16 US-10-437-963-183003	Sequence 183003,

14	510.5	32.5	810	15	US-10-425-114-37579	Sequence 37579, A
15	506.5	32.2	802	17	US-10-425-115-350231	Sequence 350231,
16	497.5	31.6	192	16	US-10-767-701-36700	Sequence 36700, A
17	451	28.7	536	9	US-09-813-718-2	Sequence 2, Appli
18	451	28.7	536	15	US-10-240-532-2	Sequence 2, Appli
19	451	28.7	536	16	US-10-240-527A-2	Sequence 2, Appli
20	450	28.6	528	17	US-10-370-715B-372	Sequence 372, App
21	440.5	28.0	301	10	US-09-919-039-132	Sequence 132, App
22	430.5	27.4	178	9	US-09-813-718-6	Sequence 6, Appli
23	430.5	27.4	178	15	US-10-240-532-6	Sequence 6, Appli
24	430.5	27.4	178	16	US-10-240-527A-6	Sequence 157861,
25	412	26.2	299	15	US-10-424-599-157861	Sequence 44089, A
26	407.5	25.9	423	16	US-10-767-701-44089	Sequence 109255,
27	402	25.6	409	16	US-10-437-963-109255	Sequence 197042,
28	389.5	24.8	351	17	US-10-425-115-197042	Sequence 53595, A
29	378	24.0	267	15	US-10-425-114-53595	Sequence 327897,
30	378	24.0	267	17	US-10-425-115-327897	Sequence 361131,
31	370.5	23.6	141	17	US-10-425-115-361131	Sequence 240858,
32	369	23.5	256	15	US-10-424-599-240858	Sequence 41506, A
33	366	23.3	254	16	US-10-767-701-41506	Sequence 163246,
34	337.5	21.5	185	16	US-10-437-963-163246	Sequence 283649,
35	315.5	20.1	217	17	US-10-425-115-283649	Sequence 22, Appl
36	293	18.6	58	9	US-09-813-718-22	Sequence 22, Appl
37	293	18.6	58	15	US-10-240-532-22	Sequence 22, Appl
38	293	18.6	58	16	US-10-240-527A-22	Sequence 304067,
39	291.5	18.5	364	17	US-10-425-115-304067	Sequence 197045,
40	253	16.1	158	17	US-10-425-115-197045	Sequence 157860,
41	233	14.8	307	15	US-10-424-599-157860	Sequence 44568, A
42	225	14.3	690	15	US-10-282-122A-44568	Sequence 202020,
43	197	12.5	109	15	US-10-424-599-202020	Sequence 287402,
44	193.5	12.3	113	17	US-10-425-115-287402	Sequence 57809, A
45	188.5	12.0	669	15	US-10-282-122A-57809	

ALIGNMENTS

RESULT 1
US-09-851-026-36
; Sequence 36, Application US/09851026
; Patent No. US20020160957A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; Clauss, Matthias
; Kao, Janet
; Kayton, Mark
; Libutti, Steven K
; TITLE OF INVENTION: Endothelial Monocyte Activating
; Polypeptide II: A Mediator Which Activates Host Response
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,026
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821
; FILING DATE: 08-OCT-96
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-851-026-36

Query Match 99.7%; Score 1568; DB 9; Length 312;
Best Local Similarity 99.7%; Pred. No. 4.4e-120;
Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MANNDVAVLKRLEQKGAADQIIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60
Db 1 MANNDVAVLKRLEQKGAADQIIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60
QY 61 ELKQELIQAEIQNGVKQIAFPSPGTPHANSVMSENVIQSTAVTTVSSGTEQIKGGTGDE 120
Db 61 ELKQELIQAEIQNGVKQIPFPSPGTPHANSVMSENVIQSTAVTTVSSGTEQIKGGTGDE 120
QY 121 KKAKEKIEKKGEKKEKQOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEVD 180
Db 121 KKAKEKIEKKGEKKEKQOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEVD 180
QY 181 VGEIAPRTVVSGLVNHPVLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
Db 181 VGEIAPRTVVSGLVNHPVLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
QY 241 PPNCGSVPGDRITFDAPFGPEPKELNPKKKIWEQIQPDLHTNDECVAITYKGVFPFVKGV 300
Db 241 PPNCGSVPGDRITFDAPFGPEPKELNPKKKIWEQIQPDLHTNDECVAITYKGVFPFVKGV 300
QY 301 CRAFTMSNSGIK 312
Db 301 CRAFTMSNSGIK 312

RESULT 2
US-09-851-026-35
Sequence 35, Application US/09851026
Patent No. US20020160957A1
GENERAL INFORMATION:

APPLICANT: Stern, David M.
Claus, Matthias
Kao, Janet
Kayton, Mark
Libutti, Steven K

TITLE OF INVENTION: Endothelial Monocyte Activating

Polypeptide II: A Mediator Which Activates Host Response

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,026
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/360,821

FILING DATE: 08-OCT-96
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-851-026-35

Query Match 85.4%; Score 1343; DB 9; Length 310;
Best Local Similarity 85.9%; Pred. No. 1.2e-101;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;

QY 1 MANNDVAVLKRLEQKGAADQIIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60
Db 1 MANNDVAVLKRLEQKGAADQIIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60
QY 61 ELKQELIQAEIQNGVKQIAFPSPGTPHANSVMSENVIQSTAVTTVSSGTEQIKGGTGDE 119
Db 61 ELKQELIQAEIQNGVKQIAFPSPGTPHANSVMSENVIQSTAVTTVSSGTEQIKGGTGDE 119
QY 120 EKAKEKIEKKGEKKEKQOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEV 179
Db 120 EKAKEKIEKKGEKKEKQOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEV 179
QY 180 DVGEIAPRTVVSGLVNHPVLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEIL 239
Db 180 DVGEIAPRTVVSGLVNHPVLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEIL 239
QY 240 APPNGSVPGDRITFDAPFGPEPKELNPKKKIWEQIQPDLHTNDECVAITYKGVFPFVKGV 299
Db 240 APPNGSVPGDRITFDAPFGPEPKELNPKKKIWEQIQPDLHTNDECVAITYKGVFPFVKGV 299
QY 300 VCRAFTMSNSGIK 312
Db 300 VCRAFTMSNSGIK 312

RESULT 3
US-09-851-026-11
Sequence 11, Application US/09851026
Patent No. US20020160957A1
GENERAL INFORMATION:

APPLICANT: Stern, David M.
Claus, Matthias
Kao, Janet
Kayton, Mark
Libutti, Steven K

TITLE OF INVENTION: Endothelial Monocyte Activating

Polypeptide II: A Mediator Which Activates Host Response

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30, Version #1.30
CURRENT APPLICATION DATA:

[illegible]

Query Match	45.1%	Score 703	Length 117
Best Local Similarity	100.0%	Pred. No. 3.8e-50	
Matches 147	Conservative	0	Mismatches 0
			Indels

QY	1	MANNDAVLKRLREQGAEDQIIEYLKQQVSLLLKEKAILQATLREKKLRVENAKLKKEIE	60
Dd	1	MANNDAVLKRLREQGAEDQIIEYLKQQVSLLLKEKAILQATLREKKLRVENAKLKKEIE	60
QY	61	ELKQELIQAEIQNGVKQIAFPSPGTPLHANSVMSENVIQSTAVTTVSSGTKEQIKGGTGDE	120
Dd	61	ELKQELIQAEIQNGVKQIAFPSPGTPLHANSVMSENVIQSTAVTTVSSGTKEQIKGGTGDE	120
QY	121	KKAKEKTEKKGEKKEKKQQSIAGSADS	147
Dd	121	KKAKEKTEKKGEKKEKKQQSIAGSADS	147

```

RESULT 7
US-10-823-730-1
; Sequence 1, Application US/10823730
; Publication No. US20040185060A1
; GENERAL INFORMATION:
; APPLICANT: IMAGENE CO., LTD.
; TITLE OF INVENTION: Immunological enhancement agent comprising N-terminal peptide of
; TITLE OF INVENTION: p43 as an effective component
; FILE REFERENCE: NPFI918
; CURRENT APPLICATION NUMBER: US/10/823,730
; CURRENT FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 1
; LENGTH: 147
; TYPE: PRT
; ORGANISM: mammalian
US-10-823-730-1

```

Query Match	45.1%;	Score 709;	DB 16;	Length 147;
Best Local Similarity	100.0%;	Pred. No. 3.8e-50;		
Matches 147;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MANNDAVLKRLEQKGAEADQIIIEYLKQOVSLIKEKAILQATLREKKLRVENAKLKEIE	60	
Db	1	MANNDAVLKRLEQKGAEADQIIIEYLKQOVSLIKEKAILQATLREKKLRVENAKLKEIE	60	
Qy	61	ELKQELIQAEIONGVKQIAFPSTGPLHANSMVSENVIOSTAVTTVSSGTKEQIKGGTGDE	120	
Db	61	ELKQELIQAEIONGVKQIAFPSTGPLHANSMVSENVIOSTAVTTVSSGTKEQIKGGTGDE	120	
Qy	121	KKAKEKIEKKGEKKKQSQIAGSADS	147	
Db	121	KKAKEKIEKKGEKKKQSQIAGSADS	147	

RESULT 8
US-10-424-599-180396
; Sequence 180396, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 180396
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; , OTHER INFORMATION: Clone ID: PAT_MRT3847_133912C.1.1.pep
US-10-424-599-180396

Query Match	33.6%;	Score 528;	DB 15;	Length 353;
Best Local Similarity	43.6%;	Pred. No. 8.6e-35;		
Matches 113; Conservative	41;	Mismatches 79;	Indels 26;	Gaps 4

Qy	56	KKEIEELKQELIQAEIQNGVKQIAFPSSGTPPLHANSMVSENVIQSTAVTTVSSGTEQIKG	115
		: : : : : : : : : : : :	
Db	119	KPLFRELKDE---EVEFYRKKFAGSQADRIVRAEAEQAQNVAEQLKTKKVSDGNGKKKPG	174
		: : : : : : : : : : : : : : : :	
Qy	116	GTGDEKKAKEKIEKKGEKKQKQSIAGSADSKPIDVSRDLRLRIGCIITARKHPDADSLY	175
		: : : : : : : : : : : : : : : : : : : :	
Db	175	KSSNEAKNK-----AAAEPDITITRLDIRVGLIICKAQKHPDADALY	215
		: : : : : : : : : : : : : : : : : : : :	
Qy	176	VEEVDVGEIAPRTTVVSGLVNHVPLEQMONRMVILLCNLKPAMRGVLSQAMVMCASSPE -	234
		: : : : : : :	
Db	216	VEEIDVGEEQTRTVVSGLVKFIPLDEMQRKVCVLCNLKPFVTRMGIKSQAMVLAASDGDH	275
		: : : : : : : : : : : : : :	
Qy	235	-KIEILAPPNGSVPGDRITFDFAFPGEPPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPF	293
		: : : : : : : : : : : : : :	
Db	276	TKVELVEPPSSAQGGERITFPGYEGNPDELLNPKKKVWETLQVDLHTNEELVACYKQNVPL	335
		: : : : : : : : : : : : : :	
Qy	294	EVKGGKVCRAQTMSNSGIK	312
		: : : : : : : : : : : : : : : :	
Db	336	TTSA-GVCKVSSISCSIR	353
		: : : : : : : : : : : : : : : :	

RESULT 9
 US-10-425-115-350232
 ; Sequence 350232, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 350232
 ; LENGTH: 377
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(377)
 ; OTHER INFORMATION: unsure at all xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_82583C.1.pep
 US-10-425-115-350232

Query Match	32.9%;	Score 517.5;	DB 17;	Length 377;
Best Local Similarity	38.2%;	Pred. No. 6.8e-34;		
Matches 122;	Conservative 50;	Mismatches 84;	Indels 63;	Gaps 11
Qy	18	ADQIIEYLKQOVSLLEKKAIIQATLREEKKLRVENAKLKKE-----IEE	61	
Db	98	SDEVL-----RQNLSPSENL---SLSEKKG---EIAKAKSPWDFVAGHRIGKPAPLFKE	147	
Qy	62	LKQELIQAEIQNGVKQIAFPSPGTPHLHANSVMVSENVIOSTAVTTVSSGTK--EQIKGGTGD	119	
Db	148	LKDE-----DVALHREKYAGSQAERSSKAAADAEANKVANQLKG----	186	
Qy	120	EKKAKEIEKKGEKKQKQSIAGSADSKPID----VSRLLDLRIGCIIITARKHPDADSLY	175	
Db	187	-----TKLSDRGTKEPKQS--GGSKSTADADITVAKLDIRVGLIRKAEKHPDADSLY	239	
Qy	176	VEEVDVGEIAPRTTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLVSQAMVMCASSPE-	234	
Db	240	VEEIDVGEDTPRTTVVSGLVKFIPLEEMQNRKVCVLCNLKPVAMRGIKSHAMVLAASNEHDH	299	
Qy	235	-KIEILAPNGSVPGDRITFDAPFGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPF	293	

Db 300 TKVELVEPPESAAGVGVTFAGYSGEPEASLSGKSKTWEKLAELHNSGELVACYKDVFP 359

QY 294 EVKGGVCVCRQAQTMSNSGIK 312

Db 360 TTSA-GICKVKTIANGEIR 377

RESULT 10

US-10-437-963-183001

; Sequence 183001, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 183001

; LENGTH: 804

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_80132C.1.pap

US-10-437-963-183001

Query Match 32.9%; Score 517; DB 16; Length 804;

Best Local Similarity 38.1%; Pred. No. 2.1e-33;

Matches 117; Conservative 53; Mismatches 79; Indels 58; Gaps 9;

QY 35 KAILQATLREEKKL-----RVENAKLKE-----IIEELKQELIQAEIQN 73

Db 527 EVLLQLNMTPEESLSFCDDKGEIAKAKRPWDFVSAGHKIGKPSPLFKELKDEEVES---- 582

QY 74 GVKQIAFPSPGTPPLHANSMVSENVIOQTAVTTVSSGTK--EQIKGGTGDEKKAKEKIEKKG 131

Db 583 -----FRNKFAGSQAERSSKAQADAEAKKVADKLKG-----TKLSDBG 620

QY 132 EKEKKQSQIAGSADSK---PIDVSRDLRLRIGCIITARKHPDADSLYVEEDVGEIAPR 187

Db 621 QKKEQKKQS--GSKSKNAEVDVTVAKLDIRVGLIRKAQKHPDADSLYVEEDVGEIAPR 678

QY 188 TVVSGLVNHVPLEQMQRNVILLCNLKPAKMRGVLSQLMVMCASSPE--KIEILAPPNGS 245

Db 679 TVVSGLVKFIPLHEMQNRKVCVLCNLKPVAMRGIKSHAMVLAASNEHTKVELVEPPESA 738

QY 246 VPGDRITFDAPFGEPPDKELNPKKKIWEQIQPDLHTNDECVATYKGVFPFVKGGVCRAQT 305

Db 739 AVGERVTFAGYSGEPEASLNKSKTWEKLSADLHNSGELVACYKDVFPFTTSA-GVCKVKRS 797

QY 306 MSNSGIK 312

Db 798 IASGEIR 804

RESULT 11

US-09-930-169-2

; Sequence 2, Application US/09930169

; Publication No. US20030004309A1

; GENERAL INFORMATION:

; APPLICANT: KIM, SUNGHOON

; APPLICANT: KO, YOUNG-GYU

; TITLE OF INVENTION: IMMUNOLOGICAL ENHANCEMENT AGENT COMPRISING N-TERMINAL PEPTIDE OF

; TITLE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT

; FILE REFERENCE: 058333/0106

; CURRENT APPLICATION NUMBER: US/09/930,169

; CURRENT FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: KR 2001-31310

; PRIOR FILING DATE: 2001-06-05

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: Mammalian

; OTHER INFORMATION: protein sequence

US-09-930-169-2

Query Match 32.8%; Score 516; DB 10; Length 108;

Best Local Similarity 100.0%; Pred. No. 1.6e-34;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANNDVAVLKRLEQKGAEADQIIIEYLKQOVSLKKEKAILQATLREEKKLRVENAKLKKEIE 60

Db 1 MANNDVAVLKRLEQKGAEADQIIIEYLKQOVSLKKEKAILQATLREEKKLRVENAKLKKEIE 60

QY 61 ELKQELIQAEIQNGVKQIAFPSTGPLHANSMVSENVIOQTAVTTVSSG 108

Db 61 ELKQELIQAEIQNGVKQIAFPSTGPLHANSMVSENVIOQTAVTTVSSG 108

RESULT 12

US-10-823-730-2

; Sequence 2, Application US/10823730

; Publication No. US20040185060A1

; GENERAL INFORMATION:

; APPLICANT: IMAGE CO., LTD.

; TITLE OF INVENTION: Immunological enhancement agent comprising N-terminal peptide of

; TITLE OF INVENTION: p43 as an effective component

; FILE REFERENCE: NPF1918

; CURRENT APPLICATION NUMBER: US/10/823,730

; CURRENT FILING DATE: 2004-04-14

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: Kopatentin 1.71

; SEQ ID NO 2

; LENGTH: 108

; TYPE: PRT

; ORGANISM: mammalian

US-10-823-730-2

Query Match 32.8%; Score 516; DB 16; Length 108;

Best Local Similarity 100.0%; Pred. No. 1.6e-34;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANNDVAVLKRLEQKGAEADQIIIEYLKQOVSLKKEKAILQATLREEKKLRVENAKLKKEIE 60

Db 1 MANNDVAVLKRLEQKGAEADQIIIEYLKQOVSLKKEKAILQATLREEKKLRVENAKLKKEIE 60

QY 61 ELKQELIQAEIQNGVKQIAFPSTGPLHANSMVSENVIOQTAVTTVSSG 108

Db 61 ELKQELIQAEIQNGVKQIAFPSTGPLHANSMVSENVIOQTAVTTVSSG 108

RESULT 13

US-10-437-963-183003

; Sequence 183003, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

Db 785 TTSA-GVCRVKTIANGEIR 802
|||||:|:| |:

Search completed: January 14, 2005, 16:02:35
Job time : 153 secs

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OM protein - protein search, using sw model

Run on: January 14, 2005, 15:49:22 ; Search time 40 Seconds
(without alignments)
750.491 Million cell updates/sec

Title: US-09-733-306C-4
Perfect score: 1573
Sequence: 1 MANNDVLRLEQKGAEADQ.....FEVKGKGVCRQATMSNSGIK 312
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1546	98.3	310	2 B55053	endothelial monocy
2	1343	85.4	310	2 A55053	endothelial monocy
3	564	35.9	917	2 T22898	hypothetical prote
4	499	31.7	797	2 T05247	methionine-trNA li
5	429	27.3	376	2 S64113	ARCl protein - yea
6	400.5	25.5	440	2 C84832	probable methionyl
7	343	21.8	273	2 T47822	hypothetical prote
8	223.5	14.2	722	2 B75074	methionyl-trNA syn
9	216	13.7	723	2 D71091	methionine-trNA li
10	205	13.0	616	1 SYTWT	methionine-trNA li
11	198.5	12.6	110	2 C85968	probable trNA synt
12	198.5	12.6	110	2 D91123	probable trNA synt
13	194.5	12.4	110	2 G65095	hypothetical 12.3
14	191	12.1	658	2 D69431	methionine-trNA li
15	185.5	11.8	629	2 E72297	methionine-trNA li
16	183.5	11.7	650	2 A64572	methionine-trNA li
17	182.5	11.6	651	2 F64457	methionine-trNA li
18	178.5	11.3	811	2 E71281	methionine-trNA li
19	177	11.3	660	2 E83656	methionyl-trNA syn
20	170	10.8	656	2 H71867	methionine-trNA li
21	168.5	10.7	114	2 F82090	methionyl-trNA syn
22	168.5	10.7	681	2 C75395	methionyl-trNA syn
23	168	10.7	734	2 B70173	methionine-trNA li
24	159.5	10.1	664	2 A11459	methionyl-trNA syn
25	158	10.0	664	2 S66067	methionine-trNA li
26	156.5	9.9	665	2 D95091	methionyl-trNA syn
27	156.5	9.9	679	2 H97958	methionine-trNA li
28	155.5	9.9	664	2 AB1097	methionyl-trNA syn
29	151	9.6	644	2 A97268	methionyl-trNA syn

RESULT 1
B55053
endothelial monocyte-activating protein II precursor - human
C;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Dec-2002
C;Accession: B55053
R;Kao, J.; Houck, K.; Fan, Y.; Haehnel, I.; Libutti, S.K.; Kayton, M.L.; Grikscheit, T., J.; Stern, D.M.
J. Biol. Chem. 269, 25106-25119, 1994
A;Title: Characterization of a novel tumor-derived cytokine. Endothelial-monocyte activ
A;Reference number: A55053; MUID:95014290; PMID:7929199
A;Accession: B55053
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-310 <KAO>
A;Cross-references: GB:U10117
C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)

Query Match 98.3%; Score 1546; DB 2; Length 310;
Best Local Similarity 99.0%; Pred. No. 1.9e-87;
Matches 309; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY	1	MANNDVLRLEQKGAEADQII EYLKQQVSL LKEKAILQATLR EKKLRVENAKLKEIE	60
Db	1	MANNDVLRLEQKGAEADQII EYLKQQVSL LKEKAILQATLR EKKLRVENAKLKEIE	60
QY	61	ELKQELIQAEIQNGVKQIAFPSTGPLHANSVMVSENVIQSTAVTTVSSGTKEQIKGGTGDE	120
Db	61	ELKQELIQAEIQNGVKQIRFPSTGPLHANSVMVSENVIQSTAVTTVSSGTKEQIKG--GDE	118
QY	121	KKAKEKIEKKGEKKQKQSIAGSADSKPIDVSRDLRLGICIIITARKHPDADSLYVEEVD	180
Db	119	KKAKEKIEKKGEKKQKQSIAGSADSKPIDVSRDLRLGICIIITARKHPDADSLYVEEVD	178
QY	181	VGEIAPRTVVGSLVNHVPLEQMQRNVILLCNLKPAKMRGVLSQLMVCASSPEKIEILA	240
Db	179	VGEIAPRTVVGSLVNHVPLEQMQRNVILLCNLKPAKMRGVLSQLMVCASSPEKIEILA	238
QY	241	PPNGSVPGDRITFDAPGEPDKELNPKKKIWEQIQPDLHTNDECVA TYKGVPFVKGKGV	300
Db	239	PPNGSVPGDRITFDAPGEPDKELNPKKKIWEQIQPDLHTNDECVA TYKGVPFVKGKGV	298
QY	301	CRAQTMNSGIK 312	
Db	299	CRAQTMNSGIK 310	

RESULT 2
A55053
endothelial monocyte-activating protein II precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S64113; S69425; S72274
R;Castagnoli, L.; Paoluzi, S.; Minenkova, O.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64112
A;Accession: S64113
A;Molecule type: DNA
A;Residues: 1-376 <CAS>
A;Cross-references: UNIPROT:P46672; EMBL:S72627; NID:g1322647; PIDN:CAA96812.1; PID:g1322647
A;Experimental source: strain S288C
R;Castagnoli, L.; Paoluzi, S.; Minenkova, O.
submitted to the EMBL Data Library, April 1996
A;Reference number: S69417
A;Accession: S69425
A;Molecule type: DNA
A;Residues: 1-376 <CAW>
A;Cross-references: EMBL:X97644; NID:g1310710; PIDN:CAA66247.1; PID:g1310719
R;Simos, G.; Segref, A.; Fasiolo, F.; Hellmuth, K.; Shevchenko, A.; Mann, M.; Hurt, E.C.
EMBO J. 15, 5437-5448, 1996
A;Title: The yeast protein Arc1p binds to tRNA and functions as a cofactor for the methionyl-tRNA synthetase
A;Reference number: S72274; MUID:97050848; PMID:8895587
A;Accession: S72274
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-376 <SIM>
A;Cross-references: EMBL:X95481; NID:g1620459; PIDN:CAA64750.1; PID:g1620460
C;Genetics:
A;Gene: SGD:ARC1; G4P1
A;Cross-references: MIPS:YGL105w; SGD:S0003073
A;Map position: 7L
C;Complex: homodimer
C;Function:
A;Description: functions as a cofactor for methionyl- and glutamyl-tRNA synthetases
C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)
C;Keywords: cytosol; homodimer

Query Match 27.3%; Score 429; DB 2; Length 376;
Best Local Similarity 42.7%; Pred. No. 3.7e-19;
Matches 105; Conservative 32; Mismatches 81; Indels 28; Gaps 9;

Qy 56 KKEIE---ELKQELIQAEIQNGVKQIAPPSGTPHANSMVSENIQSTAVTTVSSGKTEQ 112
Db 116 KLEINHDLDPHEVIE-----KKKAPAGGAADAANKADEVSK-----KAKQD 160

Qy 113 IKGGTGDE--KKAKEKIE-KKGEKK--EKQOSIAGSADSKPIDVSRDLRIGCIITA 165
Db 161 HPRGKPDDETLKCLREEAKAKAAKKAANAKQQEQQKAPKP-KPSAIDFRVGFQKA 219

Qy 166 RKHPDADSLYVEEDVG-EIAPRTVSGLVNHVPLEQMQRNVILLCNLKPAMRGVLSQ 224
Db 220 IKHPDADSLYSTIDVGDEEGPRTVCSGLVKHFLDAMQERYVVVVCNLPVNMRIKST 279

Qy 225 AMVMCASSPEKIEILAPPNGSVPGDRITFDAPPGE-PDKELNPKKIWEIQIPDLHTNDE 283
Db 280 AMVLCGSDNDKVEFVEPPKOSKAGDKVFEFGFGDEAPMKQLNPKKKIWEHLQPHFTTNDG 339

Qy 284 CVATYK 289
Db 340 LEVIFK 345

RESULT 6
C84832
probable methionyl-tRNA synthetase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84832
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84832
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-440 <STO>
A;Cross-references: UNIPROT:Q7XJM9; GB:AE002093; NID:g4895232; PIDN:AAD32818.1; GSPDB:G1322647
C;Genetics:
A;Gene: At2g40660
A;Map position: 2
C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)

Query Match 25.5%; Score 400.5; DB 2; Length 440;
Best Local Similarity 35.6%; Pred. No. 2.5e-17;
Matches 105; Conservative 45; Mismatches 86; Indels 59; Gaps 9;

Qy 22 IEYLKQVSLKKEKAILQATLRE-----EKKLRVE-NAKLKKEIEELKQELIQAEIQNG 74
Db 180 VNYIQNKEELSTLFAPIPVKLPFFSFEVPPKPAIKVETNSNSKAAE-----G 226

Qy 75 VKQIAPPSGTPHANSMVSENIQSTAVTTVSSGKTEQIKGGTGDEKKAKIEKKGEKK 134
Db 227 VKPVDKPDVQP-----OLGTKK-----TEPEPKNAAKEKDAKK 261

Qy 135 EKKQOSIAGSADSKP-----IDVSRDLRIGCIITARKHPDADSLYVEEDVGEIAPRT 188
Db 262 EKKK-----PAPEPAKKEAELSVSLNIQVGLIRKAWKHPADSLLVEEDVGEDKVRQ 316

Qy 189 VVSGLVNHVPLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPEK--IEILAPPNGSV 246
Db 317 VVSGLAKFCSPEDLTNRLVALITNVKPGKLRDVMVMSQGLVLCASSEDHSHVVEPLLPAGAK 376

Qy 247 PGDRITFDAPPGEKELNPKKIWEIQIPDLHTNDECVATYKGVPPFEVKGKGV 301
Db 377 PGERVSFSGIEGKPEDVLPNPKKQLEKITPGLYTDENGVAITYKGIQF-MTSAGPC 430

RESULT 7
T47822
hypothetical protein F24G16.250 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 17-Feb-2003
C;Accession: T47822
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24477
A;Accession: T47822
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-273 <DAN>
A;Cross-references: EMBL:AL138647
A;Experimental source: cultivar Columbia; BAC clone F24G16
C;Genetics:
A;Map position: 3
A;Introns: 157/3; 226/3
A;Note: F24G16.250
C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)

Query Match 21.8%; Score 343; DB 2; Length 273;
Best Local Similarity 37.8%; Pred. No. 4.6e-14;
Matches 84; Conservative 40; Mismatches 58; Indels 40; Gaps 7;

Qy 101 AVTTVSSGKTEQIKGGTGDEKKAKIEKKGEKKQOSIAGSADSKPIDVSRDLRIG 160
Db 80 AGTTVSA-----DESEKKSE-SQKEENVKETA-----NLLDIKVG 114

Qy 161 CIITARKHPDADSLYVEEDVGEIAPRTVVSGLVNHVPLEQMQRNVILLCNLKPAMRG 220
Db 115 RIVKAWQHEEADSLYVEEDVGEAEPRICISGLVKYVPLDLLQGSVVVLANLKPRNMRG 174

Qy 221 VLSQAMVMCAS--SPEKIEILAPPNGSVPGDRITFDAPPGEKELNP-----KKK 269
Db 175 VKSCGMLLAASDAAHENVELLVPEGSVPGDRVWFG---NEEDLEQLPEPAPPNKVQKKK 231

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2005, 15:48:39 ; Search time 190 Seconds
(without alignments)
944.826 Million cell updates/sec

Title: US-09-733-306C-4
Perfect score: 1573
Sequence: 1 MANNDVLRLEQKGAEADQ.....FEVKGKGVCRQATMSNSGIK 312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1573	100.0	312	1	MCA1_HUMAN	Q12904 homo sapien
2	1362.5	86.6	359	1	MCA1_CRIGR	O54873 cricetulus
3	1343	85.4	310	1	MCA1_MOUSE	P31230 mus musculus
4	1338	85.1	319	2	Q8C2U7	Q8c2u7 mus musculus
5	1084	68.9	297	2	Q7ZWY7	Q7zw7 xenopus lae
6	671	42.7	323	2	Q9V504	Q9v504 drosophila
7	625.5	39.8	351	2	Q7Q8S7	Q7q8s7 anopheles g
8	564	35.9	917	1	SYM_CAEEL	Q20970 caenorhabdi
9	517	32.9	804	1	SYM_ORYSA	Q9zts1 oryza sativ
10	499.5	31.8	149	2	O62542	O62542 geodia cydo
11	499	31.7	797	1	SYM_ARATH	Q9svn5 arabidopsis
12	499	31.7	797	2	AAL36365	Aal36365 arabidops
13	499	31.7	797	2	AAM14393	Aam14393 arabidops
14	453.5	28.8	529	2	Q6TGS6	Q6tgs6 brachydanio
15	453.5	28.8	529	2	AAQ97863	Aaq97863 brachydan
16	451.5	28.7	529	2	O6DFZ7	O6dfz7 brachydanio
17	450	28.6	528	1	SYYC_BOVIN	Q29465 bos taurus
18	450	28.6	528	1	SYYC_HUMAN	P54577 homo sapien
19	446.5	28.4	528	1	SYYC_MOUSE	Q91wq3 mus musculus
20	441.5	28.1	373	2	Q6BY38	Q6by38 debaryomyce
21	441.5	28.1	450	2	Q9P6K7	Q9p6k7 schizosacch
22	440	28.0	528	2	Q7ZX51	Q7zx51 xenopus lae
23	439	27.9	528	2	Q6DIJ1	Q6dij1 xenopus tro
24	429	27.3	376	1	G4P1_YEAST	P46672 saccharomyc
25	429	27.3	376	2	AAS56824	Aas56824 saccharom
26	426	27.1	376	2	Q6FNN0	Q6fnn0 candida gla
27	423.5	26.9	371	2	Q754V3	Q754v3 ashbya goss
28	423.5	26.9	371	2	AAS53340	Aas53340 ashbya go
29	415	26.4	372	2	Q6CKI6	Q6cki6 kluyveromyc
30	402	25.6	409	2	Q8RUP8	Q8rup8 oryza sativ
31	401.5	25.5	394	2	Q6C763	Q6c763 yarrowia li

RESULT 1
MCA1_HUMAN
ID MCA1_HUMAN STANDARD; PRT; 312 AA.
AC Q12904; Q96CQ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Multisynthetase complex auxiliary component p43 [Contains:
DE Endothelial-monocyte activating polypeptide II (EMAP-II) (Small
DE inducible cytokine subfamily E member 1)].
GN Name=SCYE1; Synonyms=EMAP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95014290; PubMed=7929199;
RA Kao J., Houck K., Fan Y., Haehnel I., Libutti S.K., Kayton M.L.,
RA Grikscheit T., Chabot J., Nowygrod R., Greenberg S., Kuang W.J.,
RA Leung D.W., Hayward J.R., Kisiel W., Heath M., Brett J., Stern D.M.;
RT "Characterization of a novel tumor-derived cytokine. Endothelial-
RT monocyte activating polypeptide II.";
RL J. Biol. Chem. 269:25106-25119(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; U10117; AAC62202.1; --
DR EMBL; BC014051; AAH14051.1; --
DR PDB; 1E7Z; X-ray; A=147-312.
DR PDB; 1EUJ; X-ray; A/B=147-312.
DR PDB; 1FL0; X-ray; A=150-312.
DR Genew; HGNC:10648; SCYE1.
DR MIM; 603605; --
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005125; F:cytokine activity; TAS.
DR GO; GO:0000049; F:tRNA binding; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0006418; P:tRNA aminoacylation for protein translation; TAS.
DR InterPro; IPR008232; EMAP11.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002547; tRNA_bind.
DR Pfam; PF01588; tRNA_bind; 1.
DR PIRSF; PIRSF005381; EMAP11; 1.
DR PROSITE; PS50886; TRBD; 1.
DR 3D-structure; Cytokine; Protein biosynthesis; RNA-binding;
KW tRNA-binding.
FT PROPEP 1 146
FT CHAIN 147 312
FT
FT DOMAIN 151 252 Endothelial-monocyte activating
FT CONFLICT 79 79 polypeptide II.
FT HELIX 152 154 tRNA-binding.
FT STRAND 157 168 A -> P (in Ref. 2).
FT TURN 169 170
FT STRAND 171 180
FT STRAND 187 191
FT TURN 194 196
FT HELIX 199 202
FT TURN 203 204
FT STRAND 205 210
FT STRAND 216 217
FT STRAND 222 223
FT STRAND 226 227
FT STRAND 229 232
FT TURN 233 234
FT STRAND 235 238
FT STRAND 240 240
FT TURN 243 244
FT TURN 247 248
FT STRAND 250 250
FT TURN 254 255
FT TURN 266 268
FT TURN 270 270
FT HELIX 271 274
FT HELIX 275 277
FT STRAND 278 280
FT TURN 282 283
FT STRAND 285 288
FT TURN 289 290
FT STRAND 291 292
FT STRAND 294 295
FT TURN 296 298
FT STRAND 299 300
FT STRAND 302 302
FT STRAND 310 312
SQ SEQUENCE 312 AA; 34326 MW; 946310A0216F7587 CRC64;

Query Match 100.0%; Score 1573; DB 1; Length 312;
Best Local Similarity 100.0%; Pred. No. 8.5e-86;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANNDVAVLKRLEQKGAADQIIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKKEIE 60
Db 1 MANNDVAVLKRLEQKGAADQIIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKKEIE 60

QY 61 ELKQELIQAEIQGVKQIAFPSPGTPPLHANSVMSENVIQSTAVTVSSSGTKEQIKGGTGDE 120
Db 61 ELKQELIQAEIQGVKQIAFPSPGTPPLHANSVMSENVIQSTAVTVSSSGTKEQIKGGTGDE 120
QY 121 KKAKEKIEKKGEKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 180
Db 121 KKAKEKIEKKGEKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 180
QY 181 VGEIAPRTVVSLVNHVPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
Db 181 VGEIAPRTVVSLVNHVPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
QY 241 PPNGSVPGDRITFDAPFGPEPKELNPKKIWEQIOPDLHTNDECVAATYKGVPEVKGKV 300
Db 241 PPNGSVPGDRITFDAPFGPEPKELNPKKIWEQIOPDLHTNDECVAATYKGVPEVKGKV 300
QY 301 CRAQTMSNSGIK 312
Db 301 CRAQTMSNSGIK 312

RESULT 2

MCAL_CRIGR
ID MCAL_CRIGR STANDARD; PRT; 359 AA.
AC 054873;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Multisynthetase complex auxiliary component p43 [Contains:
DE Endothelial-monocyte activating polypeptide II (EMAP-II) (Small
DE inducible cytokine subfamily E member 1)].
GN Name=SCYE1;
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98070438; PubMed=9405472;
RA Quevillon S., Agou F., Robinson J.-C., Mirande M.;
RT "The p43 component of the mammalian multi-synthetase complex is likely
RT to be the precursor of the endothelial monocyte-activating polypeptide
RT II cytokine.";
RL J. Biol. Chem. 272:32573-32579(1997).
CC -1- SUBUNIT: Component of the multisynthetase complex which is
CC comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the
CC monospecific isoleucyl, leucyl, glutamyl, methionyl, lysyl,
CC arginyl, and aspartyl-tRNA synthetases as well as three auxiliary
CC proteins, p18, p48 and p43.
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
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CC -----
DR EMBL; AF021800; AAB95207.1; --
DR HSSP; Q12904; 1E7Z.
DR InterPro; IPR008232; EMAP11.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002547; tRNA_bind.
DR Pfam; PF01588; tRNA_bind; 1.
DR PIRSF; PIRSF005381; EMAP11; 1.
DR PROSITE; PS50886; TRBD; 1.
DR Cytokine; Protein biosynthesis; RNA-binding; tRNA-binding.
FT DOMAIN 198 299
SQ SEQUENCE 359 AA; 39601 MW; 4D868D1B65D72C23 CRC64;

Db 178 DVGEAAPRTVVSGLVNHVPLEQMQNRMVVLLCNLKPAMRGVLSQAMVWCASSPEKVEIL 237

QY 240 APPNGSVPGDRITFDAPPGEPEKELNPKKKIWEQIQPDLHTNDECVTATYKGVPFVEVKGKG 299

Db 238 APPNGSVPGDRITFDAPPGEPEKELNPKKKIWEQIQPDLHTNAECVTATYKGAPFVEVKGKG 297

QY 300 VCRAQTMNSNGIK 312

Db 298 VCRAQTMANSNGIK 310

RESULT 4

Q8C2U7 ID Q8C2U7 PRELIMINARY; PRT; 319 AA.

AC Q8C2U7;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430001B22 product:endothelial monocyte activating polypeptide 2, full insert sequence.

DE Name=Scyel;

GN Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NOD; TISSUE=Thymus;

RX MEDLINE=99279253; PubMed=10349636;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=NOD; TISSUE=Thymus;

RX MEDLINE=21085660; PubMed=11217851;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=NOD; TISSUE=Thymus;

RX MEDLINE=20499374; PubMed=11042159;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=NOD; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

RP SEQUENCE FROM N.A.

RC STRAIN=NOD; TISSUE=Thymus;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK087932; BAC40045.1; -.

DR HSSP; Q12904; 1EUJ.

DR MGD; MGI:102774; Scyel.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0000049; F:trna binding; IEA.

DR InterPro; IPR008994; Nucleic_acid_OB.

DR InterPro; IPR002547; trna_bind.

DR Pfam; PF01588; trna_bind; 1.

DR PROSITE; PS50886; TRBD; 1.

SQ SEQUENCE 319 AA; 35197 MW; B977E8FE742BEE6 CRC64;

Query Match 85.1%; Score 1338; DB 2; Length 319;

Best Local Similarity 85.3%; Pred. No. 8.1e-72;

Matches 267; Conservative 15; Mismatches 27; Indels 4; Gaps 3;

QY 1 MANNDVAVLKRLKQKGAEDQIIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60

Db 10 MATNDVAVLKRLKQKGAEDQIIIEYLKQVALLKEKAILQATMREKKLRVENAKLKEIE 69

QY 61 ELKQELIQAEIQGVKQIAFPSPGTPPLHANSVMVSENVIOSTAV-TTVSSGTEKQIKGGTGD 119

Db 70 ELKQELILABIHGVEQVRVRLSTPLQTNCTASESVVQSPSVATTASLATKEQIK--AGE 127

QY 120 EKKAKEKIEKKGEKKEKKQOSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEV 179

Db 128 EKKVKEKTEKKEKKE-KQSSAAASTDSKPIDASRLDLRVGCIVTAKHPDADSLYVEEV 186

QY 180 DVGEIAPRTVVSGLVNHVPLEQMQNRMVVLLCNLKPAMRGVLSQAMVWCASSPEKIEIL 239

Db 187 DVGEAAPRTVVSGLVNHVPLEQMQNRMVVLLCNLKPAMRGVLSQAMVWCASSPEKVEIL 246

QY 240 APPNGSVPGDRITFDAPPGEPEKELNPKKKIWEQIQPDLHTNDECVTATYKGVPFVEVKGKG 299

Db 247 APPNGSVPGDRITFDAPPGEPEKELNPKKKIWEQIQPDLHTNAECVTATYKGAPFVEVKGKG 306

QY 300 VCRAQTMNSNGIK 312

Db 307 VCRAQTMANSNGIK 319

RESULT 5

Q7ZWY7 ID Q7ZWY7 PRELIMINARY; PRT; 297 AA.

AC Q7ZWY7;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Scyel-prov protein.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046580; AAH46580.1; -;
DR HSSP; Q12904; 1FL0.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0000049; F:trna binding; IEA.
DR InterPro; IPR008232; EMAP11.
DR InterPro; IPR008994; Nucleic acid_OB.
DR InterPro; IPR002547; trna_bind.
DR Pfam; PF01588; trna_bind; 1.
DR PIRSF; PIRSF005381; EMAP11; 1.
DR PROSITE; PS50886; TRBD; 1.
SQ SEQUENCE 297 AA; 32510 MW; C9D40417020CAA11 CRC64;

Query Match 68.9%; Score 1084; DB 2; Length 297;
Best Local Similarity 71.9%; Pred. No. 9.4e-57;
Matches 217; Conservative 30; Mismatches 47; Indels 8; Gaps 3;

Qy 1 MANNDVLRLEQKGAEADQIIIEYLKQOVSLLEKAILQATLRREKKLRVENAKLKKEIE 60
Db ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
1 MATSNPVLNRLDQRAEADQIIIEYLKQVALLKEKAILQASVREKKLRVENAKLKKEIE 60

Qy 61 ELKQELIQAEIQNGVKQIAFPSGCTPLHANSMVSENVIQSTAVTTVSSGTEQIKGGTGDE 120
Db ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
61 VLKEQIVTTEIKNGVKQISIPTST--SADSSVSAPVSAPQAPVKSSPPAPK----SGEE 114

Qy 121 KKAKEKIEKKGEKKEKKQSQSIAGSADSKPIDVSRDLRLRIGCIITARKHPDADSLYVEVD 180
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
115 KKKKEKAEKKGEKKEKKPP--ASEDELKAVDVSRLDLRVGCIITAKKHPDADSLYVEVD 172

Qy 181 VGEIAPRTVVSGLVNHVPLEQMQRNMVILLCNLKPAKMRGVLQSAMVMCASSPEKIEILA 240
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
173 VGEATPRTVVSGLVKHIPLEQMQRNMAVLLCNLKPAKMRGILSQAMVMCASSPEKVEILD 232

Qy 241 PPNGSVPGDRITFDAPGPEPDKELNPKKIKWEIQIPDLHTNDECVATYKGVPPFEVKGKV 300
Db ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
233 PPSGAVPGDRITFQGFPGPEPDKELNPKKKTWEIQIPDLLTNDKCVATYKGAPFEVQKGC 292

Qy 301 CR 302
Db |
293 AR 294

RESULT 6

Q9V504
ID Q9V504 PRELIMINARY; PRT; 323 AA.
AC Q9V504;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG8235-PA.
GN ORFNames=CG8235;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abiril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balleson R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:

CC diphosphate + L-methionyl-tRNA (Met).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -!- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
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DR EMBL; Z73427; CAA97803.1; -.
DR PIR; T22898; T22898.
DR HSSP; Q12904; 1FLO.
DR WormPep; F58B3.5; CE06007.
DR InterPro; IPR008224; MetRS_dimerising.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002300; tRNA-synt_la.
DR InterPro; IPR001412; tRNA-synt_I.
DR InterPro; IPR002304; tRNA-synt_met.
DR InterPro; IPR009080; tRNA-synt_la_bind.
DR InterPro; IPR002547; tRNA_bind.
DR Pfam; PF00133; tRNA-synt_I; 1.
DR Pfam; PF01588; tRNA_bind; 1.
DR PIRSF; PIRSF001528; MetRS_dimerising; 1.
DR PRINTS; PR01041; TRNASYNTHMET.
DR TIGRFAMs; TIGR00398; metG; 1.
DR PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
DR PROSITE; PS50886; TRBD; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis;
KW RNA-binding; tRNA-binding.
FT SITE 44 54 "HIGH" region.
FT SITE 367 371 "KMSKS" region.
FT BINDING 370 370 ATP (By similarity).
FT DOMAIN 756 857 tRNA-binding.
SQ SEQUENCE 917 AA; 101713 MW; 3B42AABA314FBDF0 CRC64;

Query Match 35.9%; Score 564; DB 1; Length 917;
Best Local Similarity 42.3%; Pred. No. 2.7e-25;
Matches 135; Conservative 52; Mismatches 100; Indels 32; Gaps 8;

QY 1 MANNDVLRLEQKGAEDQII-EYLKQOVSLKKEKAILQATLREEKKLRVENAKLKEI 59
Db 624 MASTAAFEV-LEQGAKVISQLIAQNLLK---FDQAKALF--TRNQLRLDGENKQLTIDV 677
QY 60 EELKQELIQAEIQNGVKQIAFP--SGTPLHANSVMVSENVISQSTAVTTVSSGKQIKGGT 117
Db 678 KTLQHQLIELETAAGIKQVPKPVVSCPT-----TPTSTPASGIITE----- 718
QY 118 GDEKKAKEIEKKGEKKEKKQSIAGSADSKP-----IDVSRDLRIGCIITARKHPDADS 173
Db 719 APKKEAPSTPAPSEPKKAKEQKKGGAAPVDDTIDVGRLLDMRVGRILKCEKHPDADA 778
QY 174 LYVEEVDVGEIAPRTVWVSLVNHVPLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSP 233
Db 779 LYVEQIDVGESAPRTVWVSLVRHVPLDQMQRNLVVVLCNLKPAMRGVESRAMVMCASSP 838
QY 234 EKIEILAPPNGSVPGDRITFDAPFGPEPKELNPKKIWEIQIPDLHTNDECVATYKGVPF 293
Db 839 DKVEIMEVPADSKPGTPVVCPPYTHRPDEQLNPKKIWEITVAEDLKVSABGFAEWKGQPL 898
QY 294 EVKGGKVCRAQTMNSGIK 312
Db 899 LIGSESKMTAPTILRGVHVK 917

RESULT 9
SYM ORYSA
ID SYM ORYSA STANDARD; PRT; 804 AA.
AC Q9ZTS1;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--trNA
ligase) (MetRS).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Denizciak M., Mirande M.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA (Met) = AMP +
diphosphate + L-methionyl-tRNA (Met).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -!- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
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CC -----

DR EMBL; AF040700; AAC99620.1; -.
DR HSSP; Q12904; 1FLO.
DR Gramene; Q9ZTS1; -.
DR InterPro; IPR008224; MetRS_dimerising.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002300; tRNA-synt_la.
DR InterPro; IPR001412; tRNA-synt_I.
DR InterPro; IPR002304; tRNA-synt_met.
DR InterPro; IPR009080; tRNA-synt_la_bind.
DR InterPro; IPR002547; tRNA_bind.
DR Pfam; PF00133; tRNA-synt_I; 1.
DR Pfam; PF01588; tRNA_bind; 1.
DR PIRSF; PIRSF001528; MetRS_dimerising; 1.
DR PRINTS; PR01041; TRNASYNTHMET.
DR TIGRFAMs; TIGR00398; metG; 1.
DR PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
DR PROSITE; PS50886; TRBD; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis;
KW RNA-binding; tRNA-binding.
FT DOMAIN 4 11 Poly-Pro.
FT SITE 28 38 "HIGH" region.
FT SITE 350 354 "KMSKS" region.
FT BINDING 353 353 ATP (By similarity).
FT DOMAIN 642 745 tRNA-binding.
SQ SEQUENCE 804 AA; 89716 MW; A87E8ABBD419D440 CRC64;

Query Match 32.9%; Score 517; DB 1; Length 804;
Best Local Similarity 38.1%; Pred. No. 1.4e-22;
Matches 117; Conservative 53; Mismatches 79; Indels 58; Gaps 9;

QY 35 KAILQATLREEKKL-----RVENAKLKE-----IEELKQELIQAEIQN 73
Db 527 EVLLQLNMTPEESLSFCDDKGEIAKAKRPWDFVSAGHKIGKPSPLFKELDEEVES---- 582
QY 74 GVKQIAFPSCGTPPLHANSVMVSENVISQSTAVTTVSSGK--EQIKGGTGDEKKAKEIEKKG 131
Db 583 -----FRNKFAGSQAERSKQAQADAEAKKVADKLKG-----TKLSDGG 620
QY 132 EKKEKKQQSIAGSADSK----PIDVSRDLRIGCIITARKHPDADSLYVEEVDVGEIAPR 187
Db 621 QKKEQKQS--GGSKSKNAEVDVTVAKLDIRVGLIRKAQKHPDADSLYVEEIDVGEAPR 678
QY 188 TVVSGLVNHVPLEQMQRNVILLCNLKPAMRGVLSQAMVMCASSPE--KIEILAPPNGS 245
Db 679 TVVSGLVKFIPIEEMQNRKVCVLCNLKPVAMRGIKSHAMVLAASNEDHTKVELVEPPESA 738

DR	InterPro; IPR002547; tRNA bind.	
DR	Pfam; PF00133; tRNA-synt_1; 1.	
DR	Pfam; PF01588; tRNA_bind; 1.	
DR	PIRSP; PIRSF001528; MetRS dimerising; 1.	
DR	PRINTS; PR01041; TRNASYNTHMET.	
DR	TIGRFAMS; TIGR00398; metG; 1.	
DR	PROSITE; PS00178; AA TRNA_LIGASE_I; 1.	
DR	PROSITE; PS50886; TRBD; 1.	
KW	Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis;	
KW	RNA-binding; tRNA-binding.	
FT	SITE 26 36	"HIGH" region.
FT	SITE 348 352	"KMSKS" region.
FT	BINDING 351 351	ATP (By similarity).
FT	DOMAIN 635 738	tRNA-binding.
SQ	SEQUENCE 797 AA; 89853 MW; BOF523C2E0C1017F CRC64;	
Query Match 31.7%; Score 499; DB 1; Length 797;		
Best Local Similarity 52.9%; Pred. No. 1.7e-21;		
Matches 101; Conservative 31; Mismatches 51; Indels 8; Gaps 3;		
QY	124 KEKIEKKGEKKKKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVDVGE 183	
Db	613 KQKASSKGGGKPKPQ-----PAADREITMARLDIRVGKIVKAEKHPKADALYVEEIDVGG 667	
QY	184 IAPRTVVSGLVNHVPLEQMQRNVILLCNLKPAKRGVLSQAMVMCASSPE--KIEILAP 241	
Db	668 GEIRTVVSGLVKYIPILEEMQNRMVCVLCNLKPAKMRDIVSQAMVLAASSDGSKVLEVP 727	
QY	242 PNGSVPGDRITFDAPGEPDKELNPKKKIWEQIQPDLHTNDEC VATYKGVPFVEVKGGVC 301	
Db	728 PGTANIGERVTFPGFEGEPDDVLPNPKKVKWETLLVDLNTKENLVACYKDVFPFTTSA-GVC 786	
QY	302 RAQTMSNSGIK 312	
Db	787 KVSSISNGTIR 797	
RESULT 12		
AAL36365	PRELIMINARY; PRT; 797 AA.	
ID	AAL36365	
AC	AAL36365;	
DT	02-MAR-2004 (TrEMBLrel. 27, Created)	
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)	
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)	
DE	Putative methionyl-tRNA synthetase.	
GN	AT4G13780.	
OS	Arabidopsis thaliana (Mouse-ear cress).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.	
OX	NCBI_TaxID=3702;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,	
RA	Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,	
RA	Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,	
RA	Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,	
RA	Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,	
RA	Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,	
RA	Theologis A.;	
RT	"Arabidopsis Full Length cDNA Clones.";	
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AY064009; AAL36365.1; --	
KW	Aminoacyl-tRNA synthetase.	
SQ	SEQUENCE 797 AA; 89853 MW; BOF523C2E0C1017F CRC64;	
Query Match 31.7%; Score 499; DB 2; Length 797;		
Best Local Similarity 52.9%; Pred. No. 1.7e-21;		
Matches 101; Conservative 31; Mismatches 51; Indels 8; Gaps 3;		
QY	124 KEKIEKKGEKKKKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVDVGE 183	
Db	613 KQKASSKGGGKPKPQ-----PAADREITMARLDIRVGKIVKAEKHPKADALYVEEIDVGG 667	

QY	184 IAPRTVVSGLVNHVPLEQMQRNVILLCNLKPAKRGVLSQAMVMCASSPE--KIEILAP 241	
Db	668 GEIRTVVSGLVKYIPILEEMQNRMVCVLCNLKPAKMRDIVSQAMVLAASSDGSKVLEVP 727	
QY	242 PNGSVPGDRITFDAPGEPDKELNPKKKIWEQIQPDLHTNDEC VATYKGVPFVEVKGGVC 301	
Db	728 PGTANIGERVTFPGFEGEPDDVLPNPKKVKWETLLVDLNTKENLVACYKDVFPFTTSA-GVC 786	
QY	302 RAQTMSNSGIK 312	
Db	787 KVSSISNGTIR 797	
RESULT 13		
AAM14393	PRELIMINARY; PRT; 797 AA.	
ID	AAM14393	
AC	AAM14393;	
DT	02-MAR-2004 (TrEMBLrel. 27, Created)	
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)	
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)	
DE	Putative methionyl-tRNA synthetase.	
GN	AT4G13780.	
OS	Arabidopsis thaliana (Mouse-ear cress).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.	
OX	NCBI_TaxID=3702;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,	
RA	Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,	
RA	Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,	
RA	Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,	
RA	Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,	
RA	Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,	
RA	Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,	
RA	Davis R.W., Ecker J.R., Theologis A.;	
RT	"Arabidopsis Open Reading Frame (ORF) Clones.";	
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AY091454; AAM14393.1; --	
KW	Aminoacyl-tRNA synthetase.	
SQ	SEQUENCE 797 AA; 89853 MW; BOF523C2E0C1017F CRC64;	
Query Match 31.7%; Score 499; DB 2; Length 797;		
Best Local Similarity 52.9%; Pred. No. 1.7e-21;		
Matches 101; Conservative 31; Mismatches 51; Indels 8; Gaps 3;		
QY	124 KEKIEKKGEKKKKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVDVGE 183	
Db	613 KQKASSKGGGKPKPQ-----PAADREITMARLDIRVGKIVKAEKHPKADALYVEEIDVGG 667	
QY	184 IAPRTVVSGLVNHVPLEQMQRNVILLCNLKPAKRGVLSQAMVMCASSPE--KIEILAP 241	
Db	668 GEIRTVVSGLVKYIPILEEMQNRMVCVLCNLKPAKMRDIVSQAMVLAASSDGSKVLEVP 727	
QY	242 PNGSVPGDRITFDAPGEPDKELNPKKKIWEQIQPDLHTNDEC VATYKGVPFVEVKGGVC 301	
Db	728 PGTANIGERVTFPGFEGEPDDVLPNPKKVKWETLLVDLNTKENLVACYKDVFPFTTSA-GVC 786	
QY	302 RAQTMSNSGIK 312	
Db	787 KVSSISNGTIR 797	
RESULT 14		
Q6TGS6	PRELIMINARY; PRT; 529 AA.	
ID	Q6TGS6	
AC	Q6TGS6;	
DT	05-JUL-2004 (TrEMBLrel. 27, Created)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE	Tyrosyl-tRNA synthetase.	

